

FIG. I

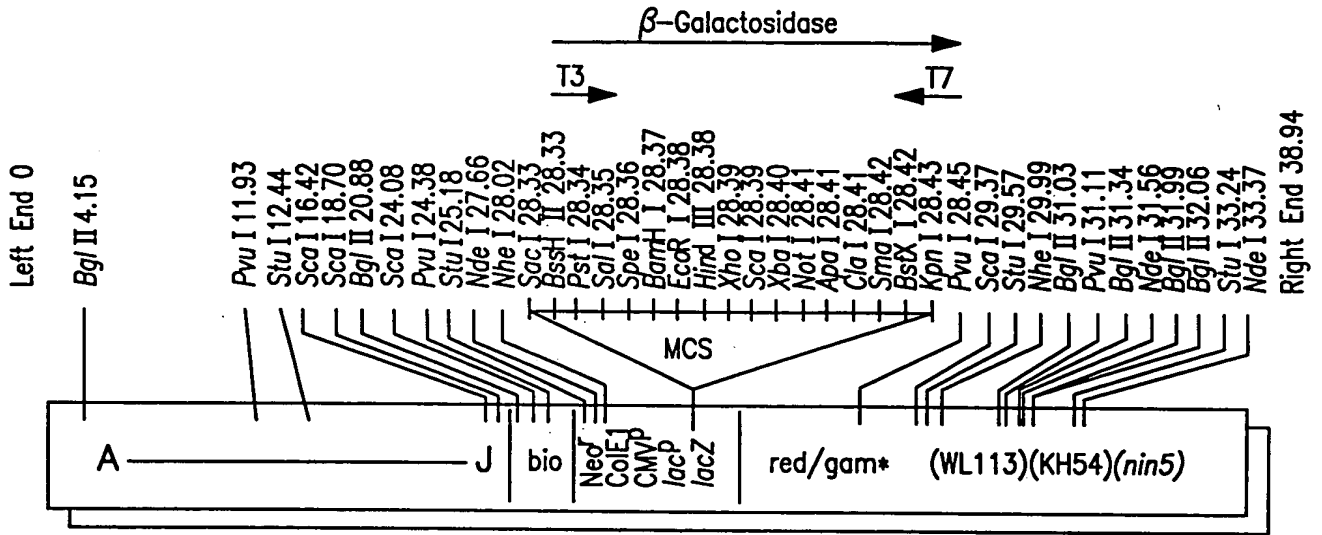


FIG. 2A

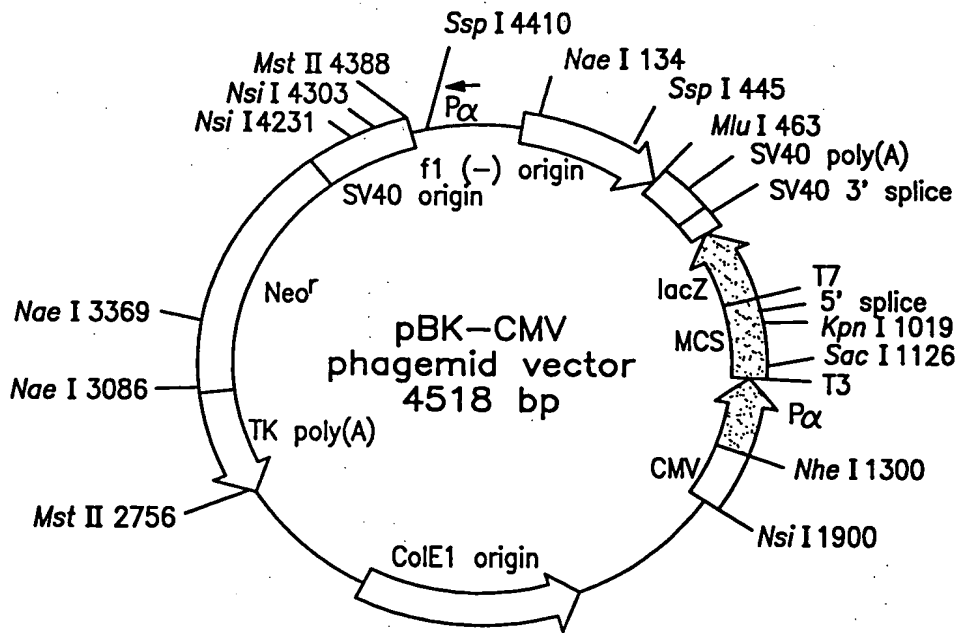


FIG. 2B

QC-RT-PCR primers for the 5' coding sequence of  
*Candida tropicalis* 20336 P450CYP52A5A

5'	ATGATTGAACAACCTCCTAGAAATATTGGTAT	GTCGTTGTGCCAGTGTGTGTACATCATCAAA	CAACTCCTTGCCATACACAAAGACTCGCGTC	3'	90
3'	TACTAACTTGTGAGGATCTTATAACCAT	CAGCAACACGGTCACAACATGTAGTAGTTT	GTTGAGGAACGTATGTGTTTCTGAGCGCAG	5'	
5'	TTGATGAAAAAGTTGGGTGCTGCCAGTC	ACAAACAAGTTGTACGACAACGGTTTCGGT	ATCGTCAATGGATGGAAGGCTCTCCAGTTC	3'	180
3'	AACTACTTTTCAACCCACGACGAGGTCAG	TGTTTGTTCACATGCTGTTCGCAAGCCA	TAGCAGTTACCTACCTTCCGAGAGGTCAG	5'	
Forward Primer 7581-97F					
5'	AAGAAGAGAGGGCAGGGCTCAAGAGTACAAC	GATTACAAGTTTGACCACTCCAAGAACCCA	AGCGTGGGCACCTACGTACGTATCTTTTTC	3'	270
3'	TTCTTTCTCCCGTCCCGAGTTCTCATGTTG	CTAATGTTCAAACTGGTGAGGTTCTTGGGT	TCCGACCCCGTGGATGCAGTCATAAGAAAG	5'	
5'	GGCACGAGGATCGTCGACCAAGATCCA	GAGAAATACAAAGCTATTTTGGCAACCCAG	TTTGGTGATTTTCTTTTGGCAAGAGGCAC	3'	360
3'	CCGTGGTCCTAGCAGCACTGGTTTCTAGGT	CTCTTATAGTTTCGATAAAACCGTTGGGTC	AAACCACTAAAAGAAACCCGTTCTCCGTC	5'	
5'	ACTCTTTTAAAGCCTTTGTTAGGTGATGGG	ATCTTCACATTGGACGGCGAAGGCTGGAAG	CACAGCAGAGCCATGTTGAGACCCACAGTTT	3'	450
3'	TGAGAAAAATTCGGAAACAATCCACTACCC	TAGAAAGTGAACCTTCCCGCTCCGACCTTC	GTGTCGTCTCGGTACAACTCTGGTGTCAAA	5'	
Reverse Primer 7581-97R					
5'	GCCAGAGAAACAAGTTGCTCATGTGACGTCG	TTGGAACCAACACTTCCAGTTGTTGAAGAAG	CATATTCTTAAGCACAAGGGTGAATACTTT	3'	540
3'	CGGTCTCTTGTTCACGAGTACACTGCAGC	AACCTTGGTGTGAAGGTCAACAACCTTCTTC	GTATAAGAATTCTGTTTCCCACTTATGAAA	5'	

FIG. 3

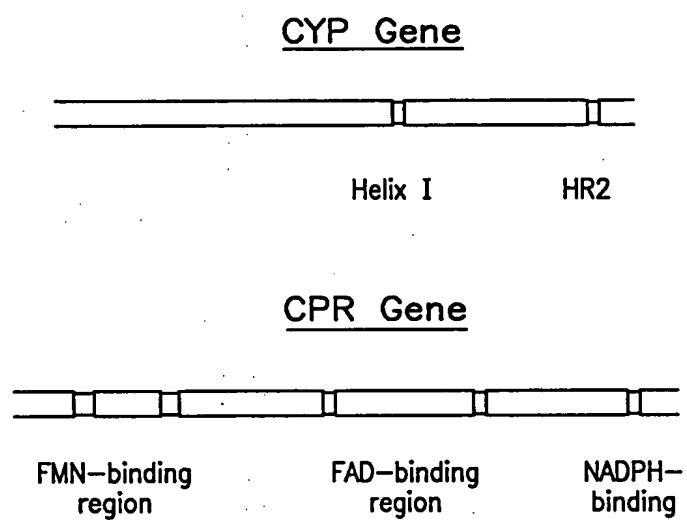


FIG. 4

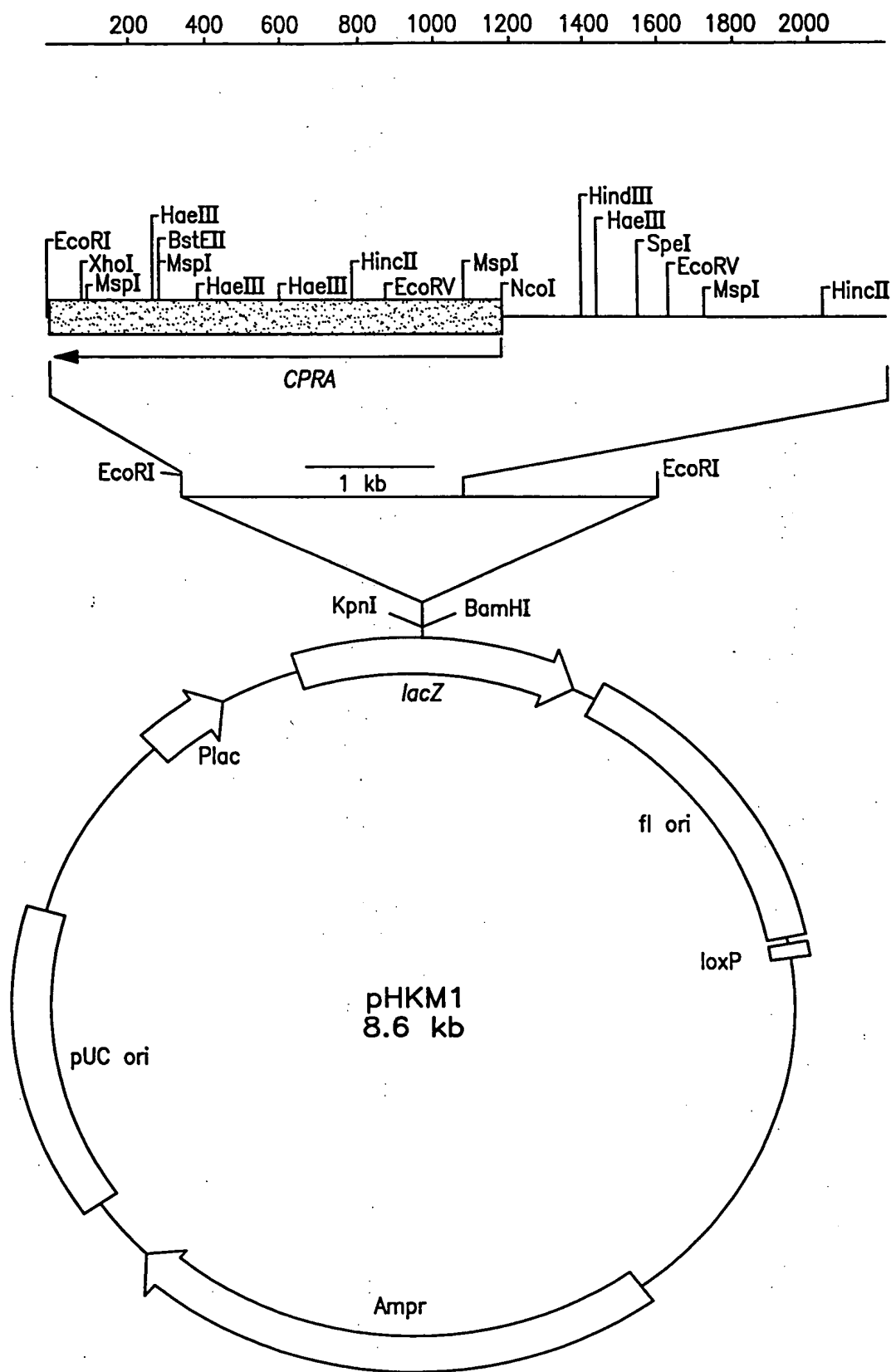


FIG. 5

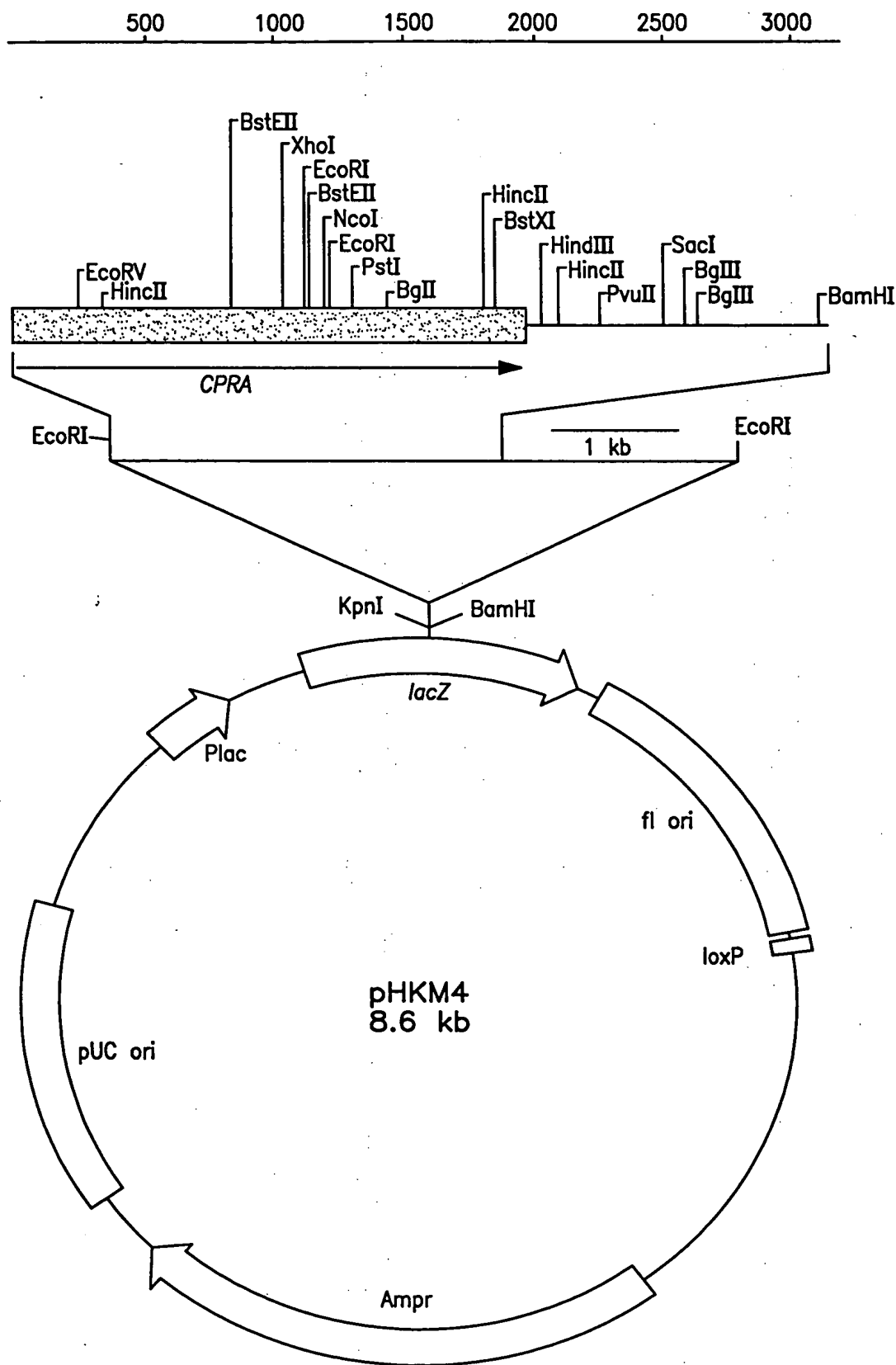


FIG. 6

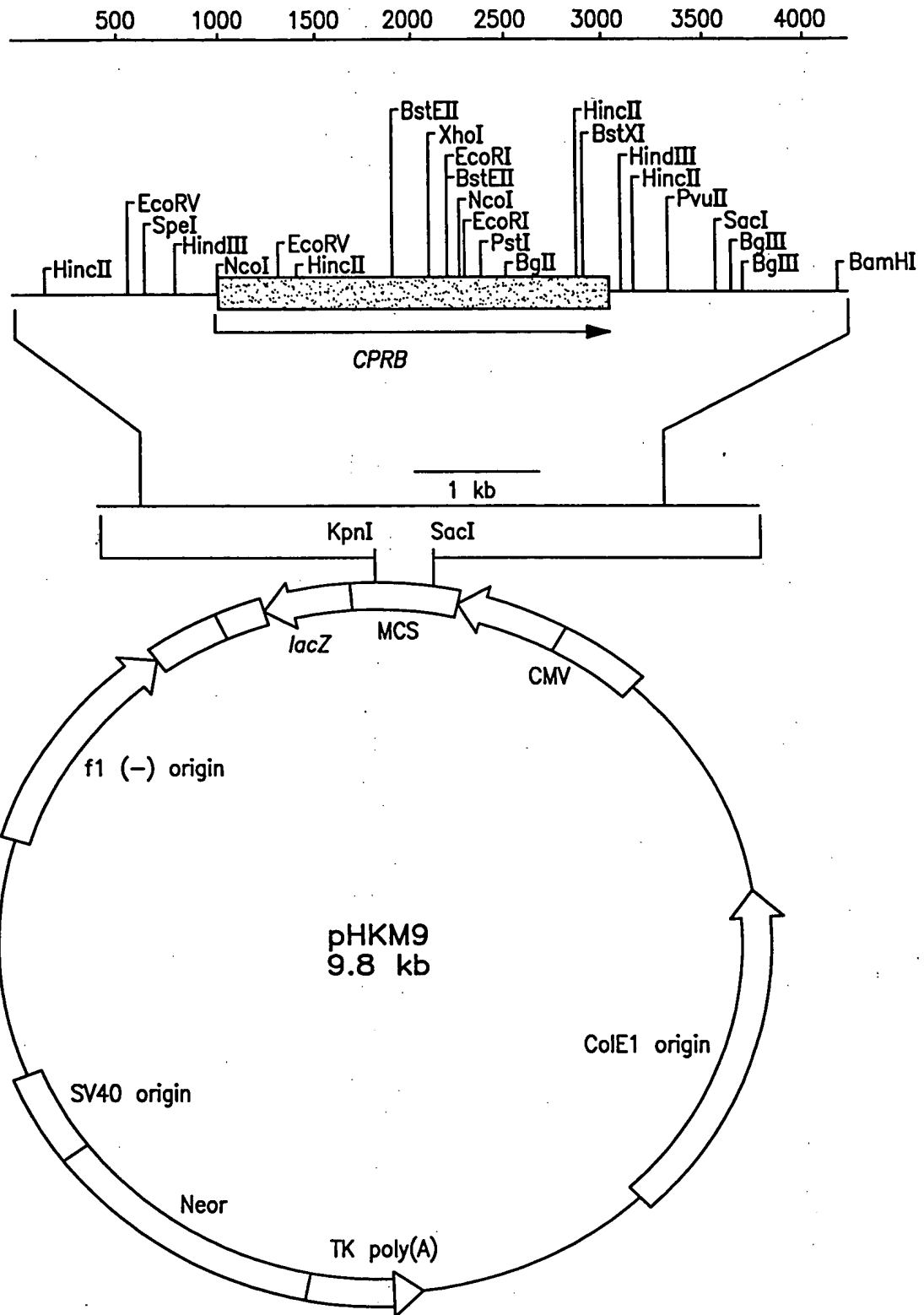


FIG. 7

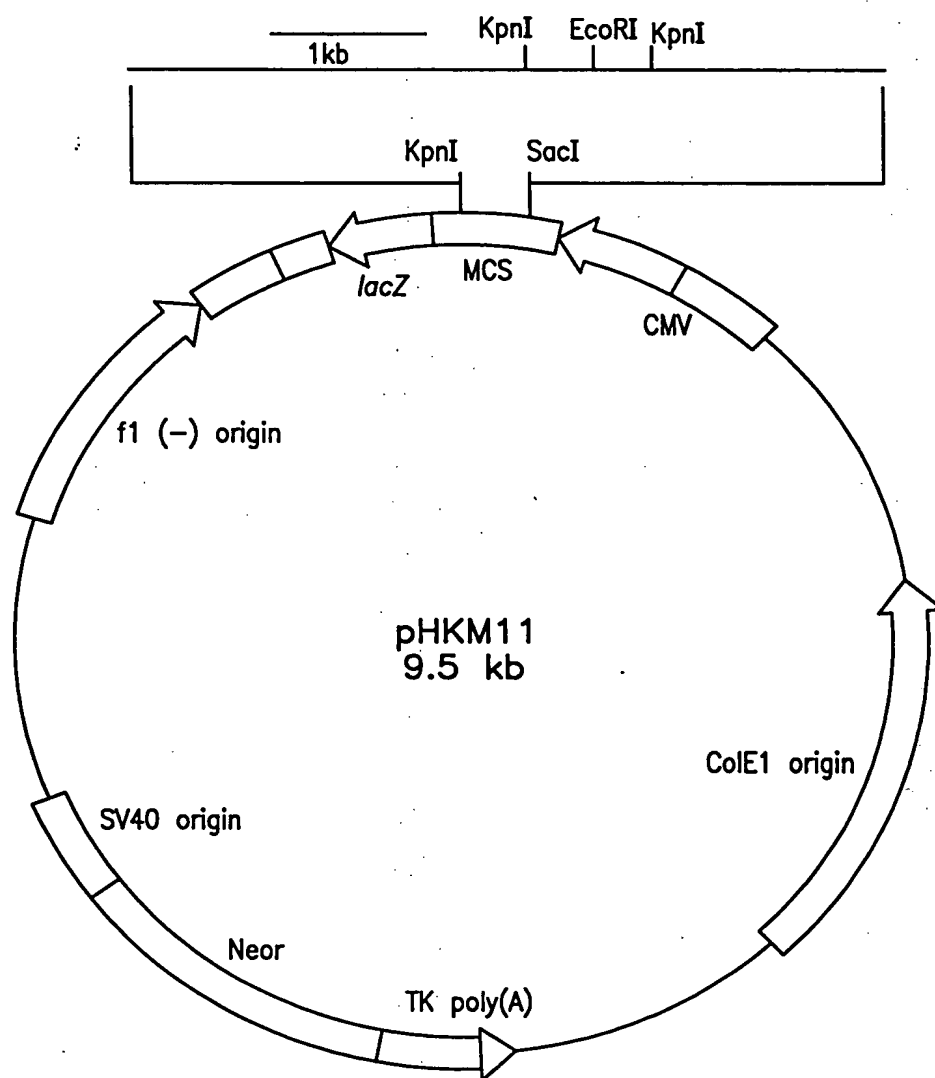
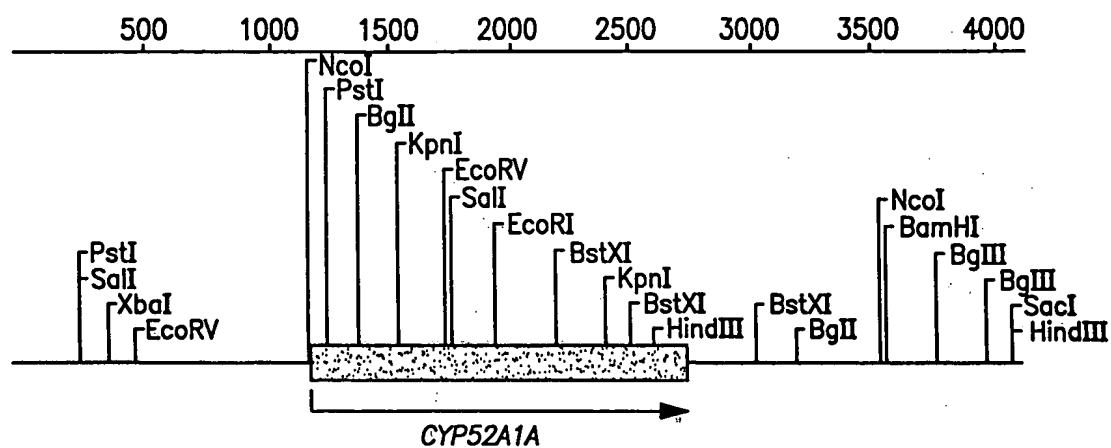


FIG. 8



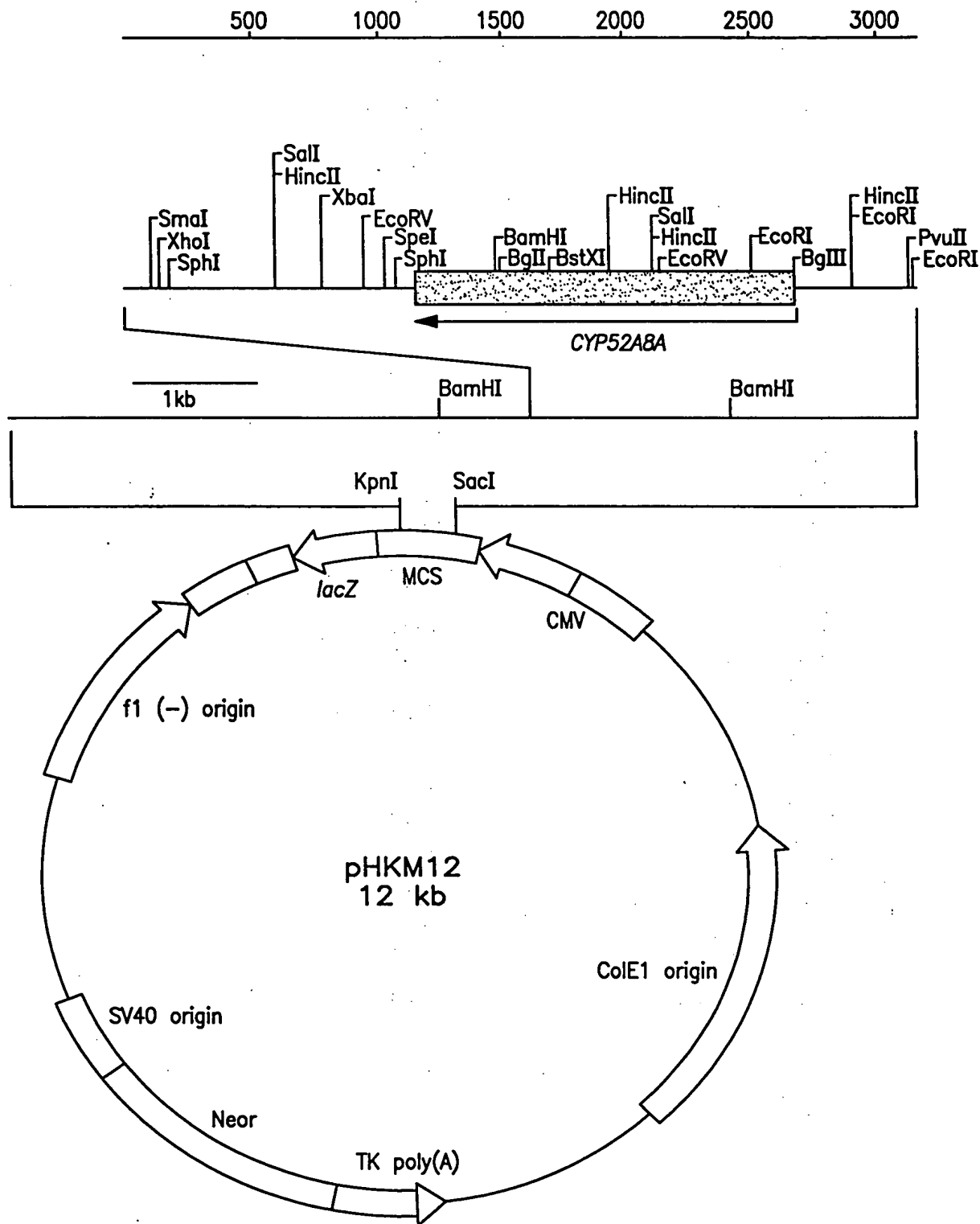


FIG. 9

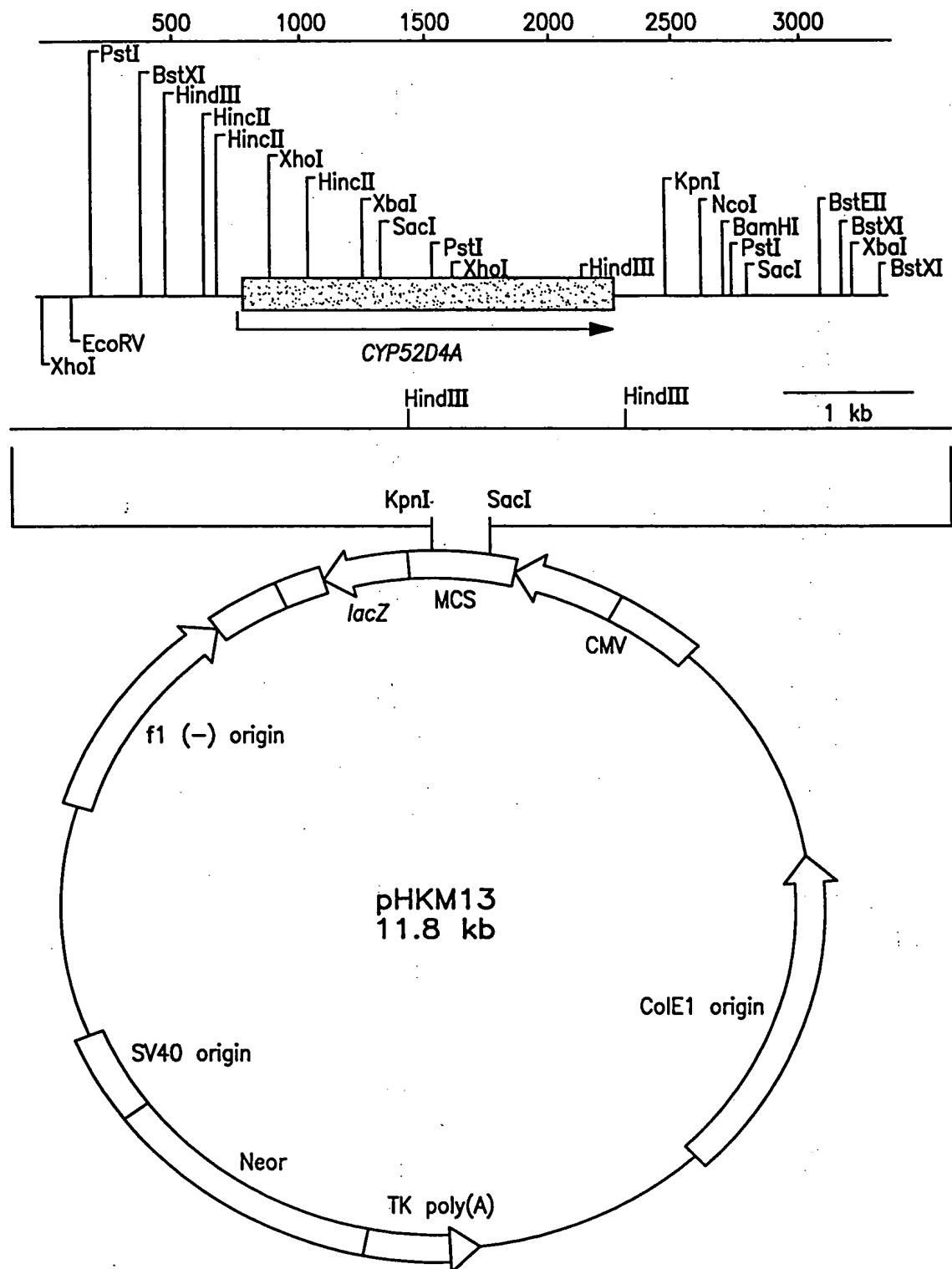


FIG. 10

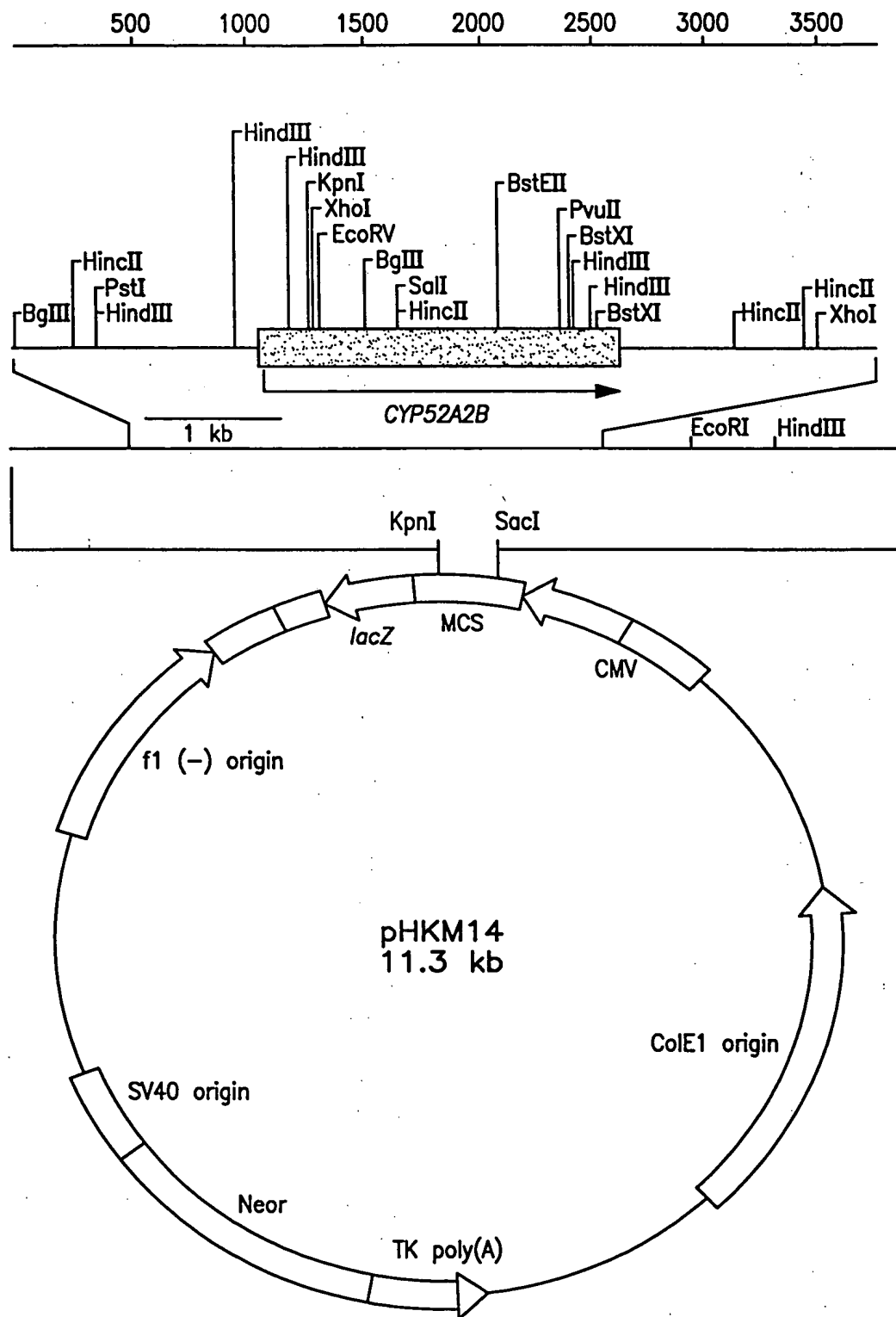


FIG. 11

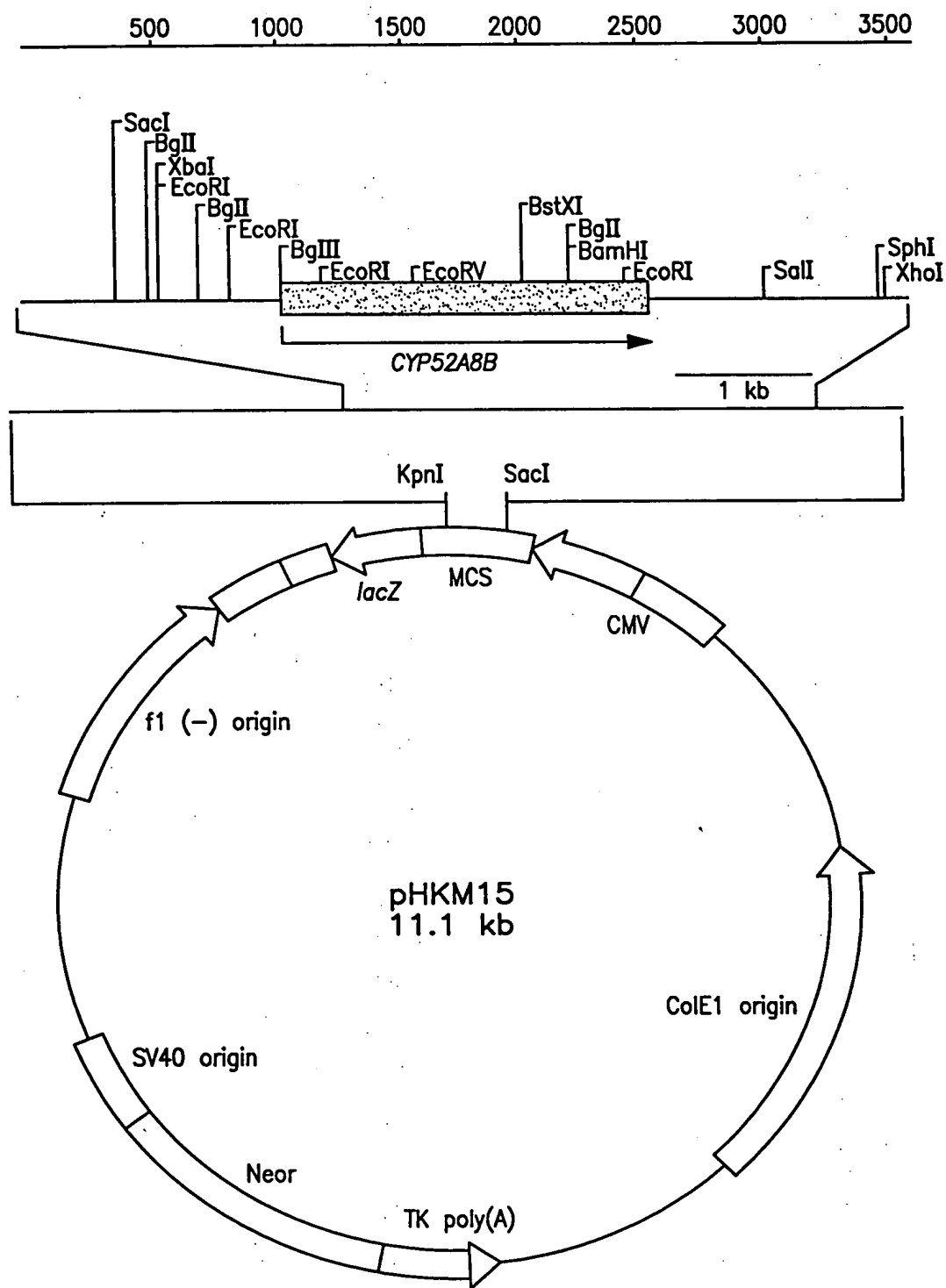


FIG. 12

*C. tropicalis* 20336 CPR Allele DNA Alignment of DS Sequence

CPRB	1	TATATGATATATATATCTTCCTGTGTAATTATTATTTCGTATTTCGTTAATACTTACTACATTTTTTT	CATCA	5
CPRB	1			70
CPRB	1		*	
CPRB	6	AGATCATCTATGGGATAATTA-----CGACAGCAACATTGCAGAAAAGAGCGTTGGTCACAATCGAAAGA		70
CPRB	71	TCCTTTATTTATGAAGAAAAGGAGAGTTCGTAAGTTGAGTTGAGTAGAATAGGCTGTGTGTCATACGGGGA		140
CPRB		* ** **** ** ** *	*** * * * * *	**
CPRB				**
CPRB	71	GCCTATG-GCGTTGCCGTCGTTGAGGCAAAATGACAGCAC--CAACAATAACGATGTTCCCGTGAAGAGC		137
CPRB	141	GCAGAGGAGAGTATCCGACGAGGAGAACTGGGTGAAATTTTCATCTATGCTGTGCGTCCCTGTACTGTAC		210
CPRB		** * * * *	** * * *	*
CPRB				*
CPRB	138	CTTCAGAAACAGTCCATTGTTGACGCT--TAAGGCACGGATAATTACGTGGGGCAAGAACGCGGAATTA		205
CPRB	211	TGTAAATCTTAGATTTCCTAGAGGTTGTTCTAGCAATAAAGTGTTCAGAGATACAATTTACAGGCAAG		280
CPRB		* * * * *	* * * *	*
CPRB				*
CPRB	206	GTTATGGGGGATCAAA--AGCGGAAGATTGTGTGTGCTTGTGGGTTTTTTCCTTTATTTTTCATATGAT		273
CPRB	281	GGTAAAGGATCAACTGATTAGCGGAAGATTGGTGTGCTGTGGGTTCTT--TTATTTTTCATATGAT		347
CPRB		* ** ** *	***** ** ** *	*****
CPRB				*****
CPRB	274	TTCTTTGCGCAAGTAACATGTGCCAATTTAGTTTGTGATTAGCGTGCC-CCACAATTGGCATCGTGGACG		342
CPRB	348	TTCTTTGCGCGAGTAACATGTGCCAATCTAGTTTATGATTAGCGTACCTCCACAATTGGCATCTTGGACG		417
CPRB		*****	***** ** *****	*****
CPRB				*****
CPRB	343	GGCGTGTTTTGTGCATACCCCAAGTCTTAACTAGCTCCACAGTCTCGACGGTGTCTCGACGATGTCTTCTT		412
CPRB	418	GGCGTGTTTTGTCTTACCCCAAGCCTTATTTAGTTCCACAGTCTCGACGGTGTCTCGCCGATGTCTTCTC		487
CPRB		*****	*** *****	*****
CPRB				*****

FIG. 13A-I

CPRA	413	CCACCCCTCCCATGAATCAATCAAGTTGTTGGGGGATCTCCACCAAGGGCACCGGAGTTAATGCTTATG	482
CPRB	488	CCACCCCTCGCAGGAATCATTCGAAGTTGTTGGGGGATCTCCTCC-----GCAGTTTATGTTTCATG	548
		***** ** ***** ** ***** ***** ** * **** ** * ****	
CPRA	483	TTTTCTCCCACTTTGGTTGTGATTGGGGTAGTCTAGTGAGTTGGAGATTTTCTTTTTTTTCGCAGGTGTCTC	552
CPRB	549	TCTTTCCCACTTTGGTTGTGATTGGGGTAGCGTAGTGAGTTGGTGATTTTCTTTTTT-CGCAGGTGTCTC	617
		* * ***** ***** ***** ***** ***** ***** ***** *****	
CPRA	553	CGATATCGAAATTTGATGAATATAGAGAGAAGCCAGATCAGCACAGTAGATTGCCCTTGTAGTTAGAGAT	622
CPRB	618	CGATATCGAAGTTTGATGAATATAG---GAGCCAGATCAGCATGGTATATTGCCCTTGTAGATAGAGAT	683
		***** ***** ***** ***** ***** ***** ***** *****	
CPRA	623	GTTGAACAGCAACTAGTTGAATTACCGCCACCACCTTGACAGCAAGTGCAGTGAGCTGTAAACGATGCAG	692
CPRB	684	GTTGAACAACAACACTAGCTGAATTACACACCCCGCT-----AAACGATGCCG	730
		***** ***** ***** ***** ***** ***** ***** *****	
CPRA	693	CCAGAGTGTCAACCACTGACCGTTGGGTGGAGTTGTTGTTGTTGGCAGGGCCATATTGCTAA	762
CPRB	731	ACAGGTGTCAACCGCCAACTGACCGTTGGGTGGAGTTG-----TTGTTGGCAGGGCCATATTGCTAA	791
		*** ***** ***** ***** ***** ***** ***** *****	
CPRA	763	ACGAAGACAAGTAGCACAAAACCCCAAGCTTAAGAACAAAAATAAAAAAATTCATACGACAATTCCAAAG	832
CPRB	792	ACGAAGAGAAGTAGCACAAAACCCCAAGTTAAGAACAA---TTAAAAAAAATTCATACGACAATTCCACAG	858
		***** ***** ***** ***** ***** ***** ***** *****	
CPRA	833	CCATTGATTACATAAT--CAACAG-TAAGACAGAAAAAACTTTCAACATTTCAAAGTTCCCTTTTTCCT	899
CPRB	859	CCATTTACATAATCAACAGCGACAAATGAGACAGAAAAAACTTTCAACATTTCAAAGTTCCCTTTTTCCT	928
		***** * ** * ** * ***** ***** ***** ***** ***** *****	

FIG. 13A-2

Cpra	900	ATTACTTCTTTTTTTTCTTCCTT-----CTTCCCTCTGTTTTTCTTACTTTATCAGTCTTTTA	962
CPRB	929	ATTACTTCTTTTTTTTCTTTCCCTTCCCTTCATTTCCCTTCTGCTTTTATTACTTTACCAGTCTTTTG	998
		***** *** ***** *****	
Cpra	963	CTTGTTTTTGCAATTCCCTCATCCTCCTCCTACTCCTCCTCACCATGGCTTTAGACAAGTAGATTGTAT	1032
CPRB	999	CTTGTTTTTGCAATTCCCTCATCCTCCTCCT-----CACCATGGCTTTAGACAAGTTAGATTGTAT	1059
		***** ***** *****	

FIG. 13A-3

FIG. 13B-1



CPRA	1523	AAGGTGGTGACAGGTTTGTCTGAATACCGCTGAAGTGATGACGGTACTGGCACCTTGGACGAAGATTTCAT	1592
CPRB	1550	AAGGTGGTGACAGATTGTCTGAATATGCTGAAGTGACGACGGCACTGGCACCTTGGACGAAGATTTCAT	1619
		*****	
		*****	
		*****	
		*****	
		*****	
CPRA	1593	GGCCTGGAAGGACAAATGTCTTTGACGCCTTGAAGAAATGAATTGAACTTTGAAGAAAAGGAATTGAAGTAC	1662
CPRB	1620	GGCCTGGAAGGATAAATGTCTTTGACGCCTTGAAGAAATGAATTGAACTTTGAAGAAAAGGAATTGAAGTAC	1689
		*****	
		*****	
		*****	
		*****	
		*****	
		*****	
CPRA	1663	GAACCAAAACGTGAAATTGACTGAGAGAGACGACTTGTCTGTCTGCTGCTGACTCCCAAGTTTCCTTGGGTGAGC	1732
CPRB	1690	GAACCAAAACGTGAAATTGACTGAGAGAGATGACTTGTCTGTCTGCCGACTCCCAAGTTTCCTTGGGTGAGC	1759
		*****	
		*****	
		*****	
		*****	
		*****	
		*****	
CPRA	1733	CAAAACAAGAAGTACATCAACTCCGAGGGCATCGACTTGACCAAGGGTCCATTTCGACCACACCCACCCATA	1802
CPRB	1760	CAAAACAAGAAGTACATCAACTCCGAGGGCATCGACTTGACCAAGGGTCCATTTCGACCACACCCACCCATA	1829
		*****	
		*****	
		*****	
		*****	
		*****	
		*****	
CPRA	1803	CTTGCCAGAAATCACCGAGACGAGAGAGTTGTTTCAGCTTCCAAGGACAGACACTGTATCCACGTTGAATTT	1872
CPRB	1830	CTTGCCAGGATCACCGAGACGAGAGAGTTGTTTCAGCTTCCAAGGAAAGACACTGTATTCACGTTGAATTT	1899
		*****	
		*****	
		*****	
		*****	
		*****	
		*****	
CPRA	1873	GACATTTCTGAATCGAACTTGAAATACACCACCGGTGACCATCTAGCTATCTGGCCATCCAACTCCGACG	1942
CPRB	1900	GACATTTCTGAATCGAACTTGAAATACACCACCGGTGACCATCTAGCCATCTGGCCATCCAACTCCGACG	1969
		*****	
		*****	
		*****	
		*****	
		*****	
		*****	
CPRA	1943	AAAACATTAAAGCAATTTGCCAAGTGTTCGGATTGGAAGATAAACTCGACACTGTTATTGAATTGAAGGC	2012
CPRB	1970	AAAACATTAAAGCAATTTGCCAAGTGTTCGGATTGGAAGATAAACTCGACACTGTTATTGAATTGAAGGC	2038
		*****	
		*****	
		*****	
		*****	
		*****	
		*****	

FIG. 13B-2

CPRA	2013	GTGGACTCCACTTACACCATCCCATCCCAACCCCAATTACCTACGGTGTGTCTATTAGACACCATTTA	2082
CPRB	2040	ATTGGACTCCACTTACACCATTCCTATCCCAACTCCAATTACTTACGGTGTGTCTATTAGACACCATTTA	2109
		*****	
CPRA	2083	GAAATCTCCGGTCCAGTCTCGAGACAATTCTTTTGTCAATTGCTGGGTTTGCTCCTGATGAAGAAACAA	2152
CPRB	2110	GAAATCTCCGGTCCAGTCTCGAGACAATTCTTTTGTGCGATTGCTGGGTTTGCTCCTGATGAAGAAACAA	2179
		*****	
CPRA	2153	AGAAAGGCTTTTACCAGACTTGGTGGTGACAAGCAAGAAATTGCCCGCCCAAGGTCAACCCGCAGAAAGTTCAA	2222
CPRB	2180	AGAAAGACTTTCACCCAGACTTGGTGGTGACAACAAGAAATTGCCCGCCCAAGGTACCCGCAGAAAGTTCAA	2249
		*****	

FIG. 13B-3

CPRB	2223	CATTGCCGATGCCCTTGTTATATTCCTCCAACAACGGCTCCATGGTCCGATGTTCCCTTTTGAATTCCCTTATT	2292
CPRB	2250	CATTGCCGATGCCCTTGTTATATTCCTCCAACAACACTCCATGGTCCGATGTTCCCTTTTGAATTCCCTTATT	2319
		*****	
CPRB	2293	GAAAAAGTTCCACACTTGACTCCACGTTACTACTCCATTTTCGTCTTCGTCAATTGAGTGAAAAAGCAACTCA	2362
CPRB	2320	GAAAAACATCCAACACTTGACTCCACGTTACTACTCCATTTTCGTCTTCGTTCGTTGAGTGAAAAAACAACACTCA	2389
		*****	
CPRB	2363	TCAACGTTACTGCAGTTGTTGAAGCCGAAGAAGAGCTGATGGCAGACCACTGCTACTGCTGTTGTTCACCAA	2432
CPRB	2390	TCAATGTTACTGCAGTCGTTGAGGCCGGAAGAAGAGCCGATGGCAGACCACTGCTACTGCTGTTGTTCACCAA	2459
		*****	
CPRB	2433	CTTGTGAAGAACGTTGAAATTTGTGCAAAAACAAGACTGGCGAAAGCCACTTGTCCACTACGATTGTGAGC	2502
CPRB	2460	CTTGTGAAGAACATTGAAATTTGCGCAAAAACAAGACTGGCGAAAGCCACTTGTTCACACTACGATTGTGAGC	2529
		*****	
CPRB	2503	GGCCCAAGAGGCAAGTTCAACAAGTTCAAGTTGCCAGTGCATGTGAGAAAGATCCAACTTTAAGTTGCCAA	2572
CPRB	2530	GGCCCAAGAGGCAAGTTCAACAAGTTCAAGTTGCCAGTGCACCGTGAGAAAGATCCAACTTTAAGTTGCCAA	2599
		*****	
CPRB	2573	AGAACTCCACCCAGTTATCTTGATTGGTCCAGGTACTGGTGTTCGCCCATTTGAGAGGTTTGTCTAG	2642
CPRB	2600	AGAACTCCACCCAGTTATCTTGATTGGTCCAGGTACTGGTGTTCGCCCATTTGAGAGGTTTGTCTAG	2669
		*****	
CPRB	2643	AGAAAGAGTTCAACAAGTCAAGAATGGTGTCAATGTTGCCAAGACTTTGTTGTTTATGTTGCAGAAAC	2712
CPRB	2670	AGAAAGAGTTCAACAAGTCAAGAATGGTGTCAATGTTGCCAAGACTTTGTTGTTTATGTTGCAGAAAC	2739
		*****	

FIG. 13C-1

CPRA	2713	TCCAACGAGGACTTTTGTACAAGCAAGAAATGGGCCGAGTACGCTTCTGTTTTGGGTGAAAACTTTGAGA	2782
CPRB	2740	TCCAACGAGGACTTTTGTACAAGCAAGAAATGGGCCGAGTACGCTTCTGTTTTGGGTGAAAACTTTGAGA	2809
		*****	
CPRA	2783	TGTTCAATGCCTTCTCCAGACAAGACCCATCCAAGAAGTTTACGTCCAGGATAAGATTTTAGAAAAACAG	2852
CPRB	2810	TGTTCAATGCCTTCTCTAGACAAGACCCATCCAAGAAGTTTACGTCCAGGATAAGATTTTAGAAAAACAG	2879
		*****	
CPRA	2853	CCAACTTGTGCA CGAGTTGTTGACTGAAGGTGCCATTATCTACGCTCTGTGGTGATGCCAGTAGAATGGCT	2922
CPRB	2880	CCAACTTGTGCA CGAGTTGTTGACCGAAGGTGCCATTATCTACGCTCTGTGGTGATGCCAGTAGAATGGCC	2949
		*****	
CPRA	2923	AGAGACGTGCAGACCAACAATTCCAAGATTGTTGCTAAAGCAGAGAAATTAGTGAAGACAAGGCTGCTG	2992
CPRB	2950	AGAGACGTCCAGACCAACGATCTCCAAGATTGTTGCCAAAGCAGAGAAATCAGTGAAGACAAGGCCGCTG	3019
		*****	
CPRA	2993	AATTGGTCAAGTCCTGGAAGGTCCAAAAATAGATACCAAGAAGATGTTTGGTAGACTCAAACGAACTCTCTC	3062
CPRB	3020	AATTGGTCAAGTCCTGGAAGGTCCAAAAATAGATACCAAGAAGATGTTTGGTAGACTCAAACGAACTCTCTC	3089
		*****	
CPRA	3063	TTTCTCCCAACGCATTTATGAATCTTTATTCTCATTTGAAGCTTTACATATGTTCTACACTTTATTTTTTT	3132
CPRB	3090	TTTCTCCCAACGCATTTATGAA---TATTCTCATTTGAAGTTTTACATATGTTCTATATTTTCATTTTTTT	3155
		*****	
CPRA	3133	TTTTTTTTTTTATTATTATACGAAACATAGGTCAACTATATATACTTGATTAAATGTTATAGAAACAA	3202
CPRB	3156	TTT-----ATTATATTACGAAACATAGGTCAACTATATATACTTGATTAAATGTTATAGAAACAA	3215
		***	

**FIG. 13C-2**

CPRA	3203	TAACTATTATCTACTCGTCTACTTCTTTGGCATTTGACATCAACATTACCGTTCCCATTTACCGTTGCCGTT	3272
CPRB	3216	TAATTATTATCTACTCGTCTACTTCTTTGGCATTTGGCATTGGCATTGGCATTGCCGTTGCCGTT	3285
		*** ****	
CPRA	3273	GGCAATGCCGGGATATTTAGTACAGTATCTCCAATCCGGATTTGAGCTATTGTAGATCAGCTGCAAGTCA	3342
CPRB	3286	GGTAATGCCGGGATATTTAGTACAGTATCTCCAATCCGGATTTGAGCTATTGTAAATCAGCTGCAAGTCA	3355
		** ****	
CPRA	3343	TTCTCCACCTTCAACCAGTACTTATACCTTCATCTTTGACTTCAAGTCCCAAGTCATAAATATTACAAGTTA	3214
CPRB	3356	TTCTCCACCTTCAACCAGTACTTATACCTTCATCTTTGACTTCAAGTCCCAAGTCATAAATATTACAAGTTA	3425
		*****	

**FIG. 13C-3**

CPRB	3413	GCAAGAACTTCTGGCCATCCACGATATAGACGTTATTACGTTATTATGCGACGTATGGATGGTTATC	3482
CPRB	3426	GCAAGAACTTCTGGCCATCCACAATATAGACGTTATTACGTTATTATGCGACGTATGGATGGTTATC	3495
		*****	
CPRB	3483	CTTATTGAACTTCTCAAACTTCAAAAACAACCCACGTCCTCCGCAACGTCATTATCAACGACAAGTTCTGG	3552
CPRB	3496	CTTATTGAACTTCTCAAACTTCAAAAACAACCCACGTCCTCCGCAACGTCATTATCAACGACAAGTTCTGA	3565
		*****	
CPRB	3553	CTCACGTCGTCGGAGCTCGTCAAGTTCTCAATTAGATCGTTCTTGTATTGATCTTCTGGTACTTCTCA	3622
CPRB	3566	CTCACGTCGTCGGAGCTCGTCAAGTTCTCAATTAGATCGTTCTTGTATTGATCTTCTGGTACTTCTCA	3635
		*****	
CPRB	3623	ATTGCTGGAACACATTTGCTCCTCGTTGTTCAAAATAGATCTTGAACAACTTTTCAACGGGATCAACTTCTC	3692
CPRB	3636	ACTGCTGGAACACATTTGCTCCTCGTTGTTCAAAATAGATCTTGAACAACTTTTCAACGGGATCAACTTCTC	3705
		*****	
CPRB	3693	AATCTGGGCCAAGATCTCCGCCCGGGATCTTCAGAAACAAGTCTGCAACCCCTGGTCGATGGTCTCCGGG	3762
CPRB	3706	GATCTGGGCCAAGATTTCCGCCCGGGATCTTCAGAAACAAGTCTGCAACCCCTGGTCGATGGTCTCCGGG	3775
		*****	
CPRB	3763	TACAAACAAGTCCAAAGGGGCAGAAAGTGTCTAGGCACGTGTTTCAACTGGTTCAACGAACATGTTTCGACAGT	3832
CPRB	3776	TACAAACAAGTCTAAAGGGGCAGAAAGTGTCTAGGCACGTGTTTCAACTGGTTCAACGAACATGTTTCGACAGT	3845
		*****	
CPRB	3833	AGTTCGAGTTATAGTTATCGTACAACCATTTTGGTTTGATTTCGAAAAATGACGGAGCTGATGCCATCAT	3902
CPRB	3846	AGTTCGAGTTATAGTTATCGTACAACCATTTTGGTTTGATTTCGAAAAATGACGGAGCTGATCCCATCAT	3915
		*****	

FIG. 13D-1

CPRB	3916	CTCCTGGTTCCTTTCATAGTACAACTGGCACTTCTTCGAGAGGCTCAATTCCCTCGTAGTTCCTCCGTCCTCAAG	3985
CPRB	3903	CTCCTGGTTCCTTTCATAGTACAACTGGCACTTCTTCGAGAGGCTCAATTCCCTCGTAGTTCCTCCGTCCTCAAG	3972
CPRB	3986	ATATTCGGCAACAAGAGCCCCGTACCGCTACGGAGCATCAAGTCGTGGCCCTGGTTGTTCAACTTGTGTA	4055
CPRB	3973	ATATTCGGCAACAAGAGCCCCGTACCGCTACGGAGCATCAAGTCGTGGCCCTGGTTGTTCAACTTGTGTA	4042
CPRB	4056	TGAAGTCCGATGTCAAGACAATCAACTGGATGTCGATGATCTGGTGGGAAACAAGTTCCTTGCATTTTAG	4125
CPRB	4043	TGAAGTCCGATGTCAAGACAATCAACTGGATGTCGATGATCTGGTGGGAAACAAGTTCCTTGCATTTTAG	4112
CPRB	4126	CTCGATGAAGTCGTACAACTCACACGTCGAGATATACCTCTGTTCCCTTCAAGAGCCGGATCCGCAAG	4182
CPRB	4183	AGCTTGTGCTTCAAGTAGTCGTTG	4145
CPRB	4146	CTCGATGAAGTCGTACAACT	

FIG. 13D-2

CPRB	MALDKLDLYVITLVAAYFAKNQFLDQPDGTGFLNTDSCNSRDVLLTLKNNKNTL	60
CPRB	MALDKLDLYVITLVAAYFAKNQFLDQPDGTGFLNTDSCNSRDVLLTLKNNKNTL	60
CPRB	LLFGSQTGTAEDYANKLSRELHSRFGGLKTMVADFADYDWDNFGDITEDILVFFIVATYGE	120
CPRB	LLFGSQTGTAEDYANKLSRELHSRFGGLKTMVADFADYDWDNFGDITEDILVFFIVATYGE	120
CPRB	GEPTDNADEFHTWLTTEADTLSTLKYTVFGLGNSTYEFFNAIGRKFDRLISEKGGDRFAE	180
CPRB	GEPTDNADEFHTWLTTEADTLSTLKYTVFGLGNSTYEFFNAIGRKFDRLISEKGGDRFAE	180
CPRB	YAEGLDGTGLDEDFMAWKDNVFDALKNDLNFEKELKYEPNVKLTERDDLSEAADSQVSL	240
CPRB	YAEGLDGTGLDEDFMAWKDNVFDALKNDLNFEKELKYEPNVKLTERDDLSEAADSQVSL	240
CPRB	GEPNKKYINSEGIDLTGPFDPHTPYLARIETRELFSSKDRHCHHVEFDISESNLKYTT	300
CPRB	GEPNKKYINSEGIDLTGPFDPHTPYLARIETRELFSSKDRHCHHVEFDISESNLKYTT	300
CPRB	GDHLAIWPSNSDENIKQFAKCFGLEDKLDTVIELKALDSTYTIPTPTITYGAVIRHHLE	360
CPRB	GDHLAIWPSNSDENIKQFAKCFGLEDKLDTVIELKALDSTYTIPTPTITYGAVIRHHLE	360
CPRB	ISGPVSRQFFLSIAGFAPDEETKKAFTRLGGDKQEFPAKVTRRKFNIAADALLYSSNNAPW	420
CPRB	ISGPVSRQFFLSIAGFAPDEETKKAFTRLGGDKQEFPAKVTRRKFNIAADALLYSSNNTPW	420
CPRB	SDVPFEFLIENVPHTLTPRYYSISSSSLSEKQLINVTAVVEAEEDGRPVTGVVTNLLKN	480
CPRB	SDVPFEFLIENVPHTLTPRYYSISSSSLSEKQLINVTAVVEAEEDGRPVTGVVTNLLKN	480

FIG. 14A



	* *		
CPRA	VEIVQNTGEKPLVHYDLSGPRGKFNKFKLPVHVRRSNFKLPKNSTTPVILIGPGTGVP	540	
CPRB	IEIAQNTGEKPLVHYDLSGPRGKFNKFKLPVHVRRSNFKLPKNSTTPVILIGPGTGVP	540	
CPRA	LRGFVRERVQQVKNGVNVGKTLIFYGCRNSNEDFLYKQEWAEYASVLGENFEMFNFSRQ	600	
CPRB	LRGFVRERVQQVKNGVNVGKTLIFYGCRNSNEDFLYKQEWAEYASVLGENFEMFNFSRQ	600	
CPRA	DPSKKVYVQDKILENSQLVHELLTEGAIYVCGDASRMARDVQTTISKIVAKSREISEDK	660	
CPRB	DPSKKVYVQDKILENSQLVHELLTEGAIYVCGDASRMARDVQTTISKIVAKSREISEDK	660	
CPRA	AAELVKS WKVQNRYQEDVW	680	
CPRB	AAELVKS WKVQNRYQEDVW	680	

FIG. 14B



CYP52A1A	60	GAACACAAATGACAACTCCTGCGTAACTTGCAAATTCCTGTGACTAAATGAAAACTCCGGACGAGTCA	129
CYP52A2A	141	CTTGTTTCGGTCAACCAATCTCTGGTGTGACCCCAATGAAGTACGCTCAACAAATTGCTGACAAAGATCTC	210
CYP52A2B	1	GCTCAACAAATTGCTCTGACAAAGATCTC	26
CYP52A3A	82	AAACTCTAGTATAATGGTGATAAAGTGGTTGCACCTCTTGCCATAGGCATGAAAAATAGGCCGTTATAGTACT	151
CYP52A3B	1		0
CYP52A5A	8	GCCAGACTTGCTCACTTTTGACTCCCTTCGAAACTCAAAGTACGTTCAGGCGGTGCTCAACGAAACGCTC	77
CYP52A5B	83	GCCAGACTTGCTCACTTTTGACTCTCTTAGAAGCTCAAAGTACGTTCAGGCGGTGCTCAACGAAACGCTT	152
CYP52A8A	1		0
CYP52A8B	1	AAAACCGATACAAGAAGAAGACAGTCAA	28
CYP52D4A	1		0
CYP52A1A	130	GACCTCCAGTCAAACGGACAGACAGACAAAACACTTGGTGGATGTTTCATACCTACAGACATGTCAACGGG	199
CYP52A2A	211	GCAACACAAAGGCTAACGCCCTGGTTGTTGAACACCGGTTGGGTTGGTTCTTCTGCTGCTAGAGGTGGTAAAG	280
CYP52A2B	27	GCAACACAAAGGCTAACGCCCTGGTTGTTGAACACACTGGTTGGGTTGGTTCTTCTGCTGCTAGAGGTGGTAAAG	96
CYP52A3A	152	ATATTAAATAAGCGTAGGAGTATAGGATGCATATGACCGGTTTTTCTATATTTTAAAGATAATCTCTAGT	221
CYP52A3B	1	CCTGCAGA	8
CYP52A5A	78	CGTATCTACCCGGGGGTACCAACGAAACATGAAGACAG--CTACGTGCAACACGACGTTGCCACGCGGAGG	145
CYP52A5B	153	CGTATCTACCCGGGGGTGCCACGAAACATGAAGACAG--CTACGTGCAACACGACGTTGCCCGCTGGAGG	220
CYP52A8A	1		0
CYP52A8B	29	CAAGAACGTTAATGTCAACCAGGCGCCAAAGAAGACGG--TTTGGCGGACTTGGAAAGATGTGGCATTTGC	96
CYP52D4A	1		0

**FIG. 15A-2**

FIG. 15A-3

CYP52A1A	200	TGTTAGACGCGGTTCTTGGCAAAGAC-AGGTGTTGGCATCTCGTACGATGGCAACTGCAGGAGGTGTCG	268
CYP52A2A	281	AGATGCTCATTTGAAGTACACCAGAGCCATTTTGGACGCTATCCACTCTGGTGAATTGTCCAAGGTTGAAT	350
CYP52A2B	97	AGATGTTCAATTGAAGTACACCAGAGCCATTTTGGACGCTATCCACTCTGGTGAATTGTCCAAGGTTGAAT	166
CYP52A3A	222	AAATTTTGTAATCTCAGTAGGATTTTCATCAAATTTTCGCAACCAATTTGCGGAAAAAATGATTCCTTTTAC	291
CYP52A3B	9	ATTGCGGGCCGTCGACAGAGTAGCAGTTATGCAAGCATGTGATTGTGGTTTTTGCACACCTGTTTGCAC	78
CYP52A5A	146	AGGCA-AAGACGGCAAGGAACCTATCT-TGGTGCAGAAGGACAGTCCGTTGGGTTGATTACTATTGCCA	213
CYP52A5B	221	AGGCA-AAGACGGTAAGGAACCTATTT-TGGTGCAGAAGGGCCAGTCCGTTGGGTTGATTACTATTGCCA	288
CYP52A8A	1		0
CYP52A8B	97	CCATG-ATGTTTATGTTCTGGAGAGGT-TTTTCAAGGAATCGTTCATCTCTCCGCCACCACAAGAACCACCA	164
CYP52D4A	1		0

FIG. 15A-3

CYP52A1A	269	ACTTCTCCTTTAGGCAATAGAAAAGACTAAGAGAAACAGCGTTTTTACAGGTTGCATTGGTTAATGTAGT	338
CYP52A2A	351	ACGAAACTTTCCCACTCTTCAACTTGAATGTCCAACTCCTGTCCAGGTGTCCCAAGTGAATCTTGAA	420
CYP52A2B	167	ACGAGACTTTCCCACTCTTCAACTTGAATGTCCAACTCCTGTCCCAAGTGTCCCAAGTGAATCTTGAA	236
CYP52A3A	292	GTCAAAAGCTGA-ATAGTGCAGTTTAAAGCACTTAAATCACATATACAGCCTCTAGATACACAGAGAA	360
CYP52A3B	79	GACAAATGATCG-ACAGT-CGATT--ACGTAATCCATATTATTAGAGGGGTAAATAAAATAAATGGCA	144
CYP52A5A	214	CGCAGACGGACCCAGAGTATTTTGGGGCCGACGCTGGTGAGTTTAAAGCCGGAGAGATGGTTTGATTCA--	281
CYP52A5B	289	CGCAGACGGACCCAGAGTATTTTGGGGCAGATGCTGGTGAGTTCAAAACCGGAGAGATGGTTTGATTCA--	356
CYP52A8A	1		0
CYP52A8B	165	GTTAACGAGATCCATATTTCACAACCCACCGCAAGGTGACAATGCTCAACAACACAGCAACAACAACA--	232
CYP52D4A	1		0
CYP52A1A	339	ATTTTTTTAGTCCCAGCATTCTGTGGGTGCTCTGGGTTTCTAGAATAAGGAAATCACAGGAGAAATGCAAA	408
CYP52A2A	421	CCCAACCAAGGCTGGACCGG-AAGGTGTTGACTCCTTCAACAAGGAAATCAAGTCTTTGGCTGGTAAGT	489
CYP52A2B	237	CCCAACCAAGGCTGGACCG--AAGGTGTTGACTCCTTCAACAAGGAAATCAAGTCTTTGGCTGGTAAGT	304
CYP52A3A	361	GCTCTTTATGATCTGAAGAAGCATTAGAATAGCT--ACTATGAGCCACTATTGGTGTATATATTAGGGA	427
CYP52A3B	145	GCC---AGAAATTCAAAACATTTTGCAACAATGCAAAAGATGAGAAACTCCAACAGAAAAATAAAAAA	210
CYP52A5A	282	AGCATGAAGAACTTGGGGTGTAATACTTGCCGTTCAATGCTGGGCCACGGACTTGTCTGGGGCAGCAGT	351
CYP52A5B	357	AGCATGAAGAACTTGGGGTGTAAGTACTTGCCGTTCAATGCTGGGCCCCCGGACTTGTCTGGGGCAGCAGT	426
CYP52A8A	1		0
CYP52A8B	233	ACCCCCACAAGAACAGTGAATAATGCCAGTCAA-CAAAGAGTGGTGACAGACGAGGGAGAAAAACGCAAG	301
CYP52D4A	1		0

FIG. 15B-I

CYP52A1A	409	TTCAGATGGAAGAACAAAGAGATAAAAAACAAAAAACTGAGTTTGCACCAATAGAAATGTTTG----	474
CYP52A2A	490	TTGCTGAAAAAC--TTCAAGACCTATGCTGACCAAGCTACCGCTGA--AGTGAGAGCTGCAGGTCCAGAAG	555
CYP52A2B	305	TTGCTGAAAAAC--TTCAAGACCTATGCTGACCAAGCTACCGCTGA--AGTTAGAGCTGCAGGTCCAGAAG	370
CYP52A3A	428	TTGGTGCAATTAAAGTACGTACTATAAACAGAGAAAAATACTTAACCAATTTCTGGTGTATACCTTAGTGG	497
CYP52A3B	211	ACTCCGCAGC--ACTCCGAACCAACAAACAAATGGGGGGGCCAG--AATTATTGAC--TATT-----	267
CYP52A5A	352	ACACTTTGATTGAAGCGAGCTACTTGCTAGTCCGGTTGGCCCGACACCTAC-CGGGCAATAGATTG----	416
CYP52A5B	427	ACACTTTGATTGAAGCGAGCTATTTGCTAGTCAGGTTGGCGCAGACCTAC-CGGGTAATCGATTTG----	491
CYP52A8A	1		0
CYP52A8B	302	CAACAGTGGTTCTGATGCAAGATCAGCTACACCGCTTCATCAGGAAAGC-AGGAGCTCCCACCAC----	366
CYP52D4A	1	GATGTGGTGCTTGATTCTCGAGACACATCCTTGTGAGGTGCCATGAATCTGTACCTG-----	58
CYP52A1A	475	-ATGATATCATCCACTCGCTAAACGAATCATGTGGGTGATCTTCTCTTTAGTTTGGTCTATCATATAAAC	543
CYP52A2A	556	CTTAAAGATATTTATTCAATTATTTAGTTTGCCTATTTATTCTCATTTACCCATC-ATCATTCAACACTAT	624
CYP52A2B	371	CTTAAAGATATTTATTCACTATTTAGTTTGCCTATTTATTTCTCATCACCCTATC-ATCATTCAACAAATAT	439
CYP52A3A	498	-TGAGGGACCTTTTCTGAACATTCGGGTCAAACTTTTTTTTGGAGTGCAGATCGATTTTTCGTTTGTGT	556
CYP52A3B	268	----GTGACTTTTTTTTATTTTTTCCGTTAA--CTTTTCATTGCAGTGAAGTGT--GTTACACGGGGTGGT	329
CYP52A5A	417	-CAGCCAGGATCGGCGTACC-CACCAAGAAAGAAAGTCGTTGATCAACATGAGTGTGCCGACGGGGTGT	484
CYP52A5B	492	-CTGCCAGGGTCGGCGTACC-CACCAAGAAAGAAAGTCGTTGATCAATATGAGTGTGCCGATGGGGTGGT	559
CYP52A8A	1		0
CYP52A8B	367	-CATATGCCCATCAGGAGCAACACAGCAGGTTAGTGTATAGTAGTCTGTAGTTAAGTCAATGCAATGTA	435
CYP52A4A	59	-TCTGTAAGCACAGGGAACCTGCTTCAACACCTTATTGCATATTTCTGTCTATTGCAAGCGTGTGTGCAAC	127

FIG. 15B-2

CYP52A1A	544	ACATGAAAGTGAAATCCAAA-TACACTACACTCCGGGTATTGTCTCTCGTTTTACAGATGTCATTGTC	612
CYP52A2A	625	ATATAAAGTTACTTCGGA-----TATCATTTGTAATCGTGCGGTGCGCAATTGGATGATTTGGAA	683
CYP52A2B	440	ATATAAAGTTATTTCGGAAC-TCATA---TATCATTTGTAATCGTGCGGTGCGCAATTGGGTAATTTGAAA	505
CYP52A3A	567	AATAATAGTGAAACCTTTGTG-TAATAAATCTTCATGCAAGACTTGCATAATTCGAGCTTGGAGTTCACG	635
CYP52A3B	330	GATGGTGTGGTTTCTACAA-TGCAAGGGCACAGTTGAAGGTTCCACATAACGT-TGCACCATATCAAC	397
CYP52A5A	485	TGT--AAAGCTTTATAAGGA-TGTAACGGTAGATGGATAGTTGTGTAGGAGGAGCGGAGATAAATTAGAT	551
CYP52A5B	560	TGT--AAAGTTTACAAAGGA-TCTAGATGGATATGTA-AGGTGTGTAGGAGGAGCGGAGATAAATTAGAT	625
CYP52A8A	1		0
CYP52A8B	436	CCA--ATAAGACTATCCCTT-CTTACAACCAAGTTTCTGCCGCGCCTGTCTGGCA-ACAGATGCTGGCC	501
CYP52D4A	128	GATATCTGCCAAGGTATATAGCAGAACGGTGCTGATGGTTCTCCTCCGGTCATATTCTGTGGTAGTTCTGCA	197

FIG. 15B-3

CYP52A1A	613	TTACTTTTGAGGTCATAGGAGTTGCCGTGTGAGAGATCACAGAGATTATCACACTCACATTTATCGTAGTT	682
CYP52A2A	684	CTGCGCTTGAAACGGATTTCATGCACGAACGGAGA-TAAAAGATTACGT---AATTATCTCCTGAGACA	749
CYP52A2B	506	CTGTAGTTGGAACGGATTTCATGCACGATCGGGAGA-TAACACG-----AGATTATCTCCTAAGACA	565
CYP52A3A	636	C--CAATTTGACCTCGTTTCATGTGATAAAAGAAAGCCAAAGGTAATT---AGCAGACGC---AATGGG	697
CYP52A3B	398	T--CAATTTATCCTCATTTTCATGTGATAAAAGAGCCAAAGGTAATT---GGCAGACCCCCCAAGGGG	462
CYP52A5A	552	TTGATTTTG---TGTAAGGTTTGGATGTCAACCTACTCCGCACCTTCATGCA-GTGTGTGTGACACAAGG	617
CYP52A5B	626	TTGATTTTG---TGTAAGGTTTAGCACGTCACGCTACTCCGCACCTTTGT-----GTGTAGGGAGCACACA---	685
			0
CYP52A8A	1		567
CYP52A8B	502	GACACACTT---TCAACTGAGTTTGGTCTAGAAATTTCTTGACATGCACGACA-AGGAAACTCTTACAAAG	266
CYP52D4A	198	GGTAAATTTGGATGTCAGGTAGTGGAGGGAGGTTTGTATCGGTTGTGTT-TTCTTCTTCCCTCTCTCTCTG	
CYP52A1A	683	TCCTATCTCATGCTGTGTGCTCTGCTGTTGGTTCATGAGTTTGGATT--GTTGTACATTAAAGGAATCGCT	750
CYP52A2A	750	ATTTTAGCCGTGTTTCACACGCCCTTCTTTGTT-CTGAGCGAAGGAT--AAATAATTAGACTTCCACAGCT	816
CYP52A2B	566	ATTTTGGCCTCATTCACACGCCCTTCTT-----CTGAGCTAAGGAT--AAATAATTAGACTTCCACAAAGTT	628
CYP52A3A	698	AACATGGAGTGGAAAGCAATGGAAGCACGCC--AGGACGGAGTAATTTAGTCCACACTACATCTGGGGGT	766
CYP52A3B	463	AACACGGAGTAGAAAGCAATGGAACACACGCC--ATGACAGTGCCCATTTAGCCCAACACACATCTAGTATT	531
CYP52A5A	618	GTGTACTACGTGTGCGCTGTGCGCCCAAGAGACA---GCCCAAGGGG--TGGTAGTGT-GTGTGGCGGAA	681
CYP52A5B	686	---TACTCCGTCTGCGCTGTGCGCCCAAGAGACG---GCCCAGGG-----TAGTGT-GTGGTGGTGAA	741
CYP52A8A	1	GAATTCCTTTGGATCTAATTCACGCTGATC---TTGCTAATCCT--TATCAACGTAAGTTGTGATCATT	62
CYP52A8B	568	--ACAACACTTGTGCTGTGATGCCACTTGATC---TTGCTAAGCCT--TATCAACGTAATTGAGATCATT	630
CYP52D4A	267	ATTCAACCTCCACGTCCTCCTTCCGGTTCTGTGTCTGTGAGTC--GTACTGTTGGATTAAATCCATC	334

FIG. 15C-1



CYP52A1A	751	GGAAAGCAAGCTAACTAAATTTTCTTTGTACAGGTACACTAACCTGTAAAACTTCACTGCCACGCCAG	820
CYP52A2A	817	CATTCTAAATTTCCGT---CACGGGAATATTGAA-----GGGGGTACATGTGGCCGCTGAA-	869
CYP52A2B	629	CATTAAATAATCCGT---CACGGGAAACTGCAACAATAAGGAAGGGGGGTAGACGTAGCCGATGAA-	694
CYP52A3A	767	-----TTTTTGTGGCAAGTACACACCTGGACT-TTAGTTTTTGCCTCCATAAAGTTAACTCTAA-	830
CYP52A3B	532	CTTTTGTGGCAGGTGCACACCTGGACT-TTAGTTATTGCCCATAAAGTTAACTCTCA-	599
CYP52A5A	682	GTGCATGTGACACA--ACGCGTGGTTCTGGCCAATGGTGGAATAAGTGCAGGTAAAGCAGCGACCTGAA	748
CYP52A5B	742	GTGCATGTGACACA--ATACCTGGTTCTGGCCAATGGGGATTTAGTGTAGGTAAAGCTGCCACCTGAA	808
CYP52A8A	63	GTTTGTCTGAATTAT--ACACACCAAGTGGAAAGAAATATGGTCTAATTTGCACGTCCCACTGGCATTTGTG--	128
CYP52A8B	631	GTTTGTCTGAATTAT--ACACACCAAGTGGAAAGAAATCTGGTCTAATCTGCACGCCCTCATGGGCATTTGTG--	696
CYP52D4A	335	GCATGTGTGAAAAAAGTAGCGCTTATTAGACAACCAAGTTCGTTGGGGGGGTATCAGAAATAGTCTGTT	404
CYP52A1A	821	TCTTTCCTGATTGGGCAAGTGCACAAACTACA-ACCTGCAAAACAG----CACTCCGCTTGTACAGGTT	885
CYP52A2A	870	-TGTGGGG--CAGTAAACGCAGTCTCTC-----CTCTCCCAGGAATAGTGCAACGG	918
CYP52ACB	695	-TGTGGGGTCCAGTAAACGCAGTCTCTCTCCCCCCCCCCCCCCCCCTCAGGAATAGTACAACGG	763
CYP52A3A	831	-CCTTTGGC-TCTCCAACCTCTCTCCGCCCCCAATAATTCGTTTTT-ACACCCCTCAAGCTAGCGACAGCAC	897
CYP52A3B	600	-CCTTTGGC-TCTCCAGTGTCTCCGCCCTCCAGATGCTCGTTTTT--ACACCCCTCGAGCTAACGACAACAC	665
CYP52A5A	749	ACATTCTCAACGCTTAAGACACTGGTGG-TAGAGATGCGGACCAGG-----CTATTCTTGTCTGCGT-GCTA	811
CYP52A5B	809	ACACTCCTCAACGCTTGAGACACTGGTGGGTAGAGATGCGGGCCAGGA--GGCTATTCTTGTCTGCGT-GCTA	875
CYP52A8A	129	-TGTTT-----GTGGGGGGGGGGGTGCACACATTTTGTAGTGCCA----TTCTTTGTGATTAC-CCCT	187
CYP52A8B	697	-TGTTT--GGGGGGGGGGGGGTGCACACATTTTGTAGTGCGAATGTTTGTGTTGCTGGTTCC-CCCT	762
CYP52D4A	405	GTGCACGACCATGAGTATGCAACTTGACGAGACGTCGTTAGGA-----ATCCACAGAATGATAGCAGGAA	469

FIG. 15C-2

CYP52A1A	886	GTCTCCTCTCAACCAACAAAAAATAAGATTAAACTTTCTTTGCTCATGCATCAATCGGAGTTATCTCTG	955
CYP52A2A	919	AGGAAGGATAACGGATAGAAAGCGGAATGCGAGGAAAT - TTTGAACGCGCAAGAAAAGCAATATCCGG	986
CYP52A2B	764	GGGAAGGATAACGGATAGCAAGTGGAATGCGAGGAAAT - TTTGAATGCGCAAGGAAAGCAATATCCGG	831
CYP52A3A	898	AACACCCATTAGAGGAATGGGCAAAAGTTAAACACTTTTGGCTTCAATGATTCCCTATTCGCTACTACATT	967
CYP52A3B	666	AACACCCATGAGGGGAATGGG - CAAAGTTAAACACTTTTGGTTTCAATGATTCCCTATTTGCTACT - - - -	729
CYP52A5A	812	CCCGCGCATGGA - AAATCAACTGCGGGAAGAA - TAAATTTATCCGTAGAAATCCACAGAGCG - - - - - G	872
CYP52A5B	876	CCCG - TGCACGGA - AAATCGATTGAGGGAAGAA - CAAATTTATCCGTGAAATCCACAGAGCG - - - - - G	935
CYP52A8A	188	CCCCCTATCAT - - - TCATTTCCACAGGATTAG - TTTTTCCTCACTGGAATTCGCTGTCC - - - - -	244
CYP52A8B	763	CCCCCTCCCCCTATCATGCCCCACAGGATTAG - TTTTTCCTCACTGGAATTCGCTGTCC - - - - -	822
CYP52D4A	470	GCTTACTACGTGAGAGATTCTGCTTAGAGGATG - TTCTCTTCTTGTGATTCCATTAGGTGGGTATCAT	537

FIG. 15C-3

CYP52A1A	956	A--AAGAGTTGCCTTTGTGTAATGTGTCCCAA--CTCAAACTGCAAAACCTAACACAGAATGAT-----	1016
CYP52A2A	987	GCTACCAGGTTTGTAGCCAGGGAACACACTCCTATTTCTGTCTCAATGACTGAACATAGAAAAA-----	1050
CYP52A2B	832	GCTATCAGGTTTGTAGCCAGGGAACACACTCCT-CTTCTGCACAAAAAATTAAACGTAGACAAAAA	900
CYP52A3A	968	CTTCTCTTGTGTTGTGCTTTGAATTGCACCATGTGAAATAAACGACAATTATATATACCTTTTCATC---	1034
CYP52A3B	730	---CTCTTGTGTTTGTGTTTGTGTTTGTGACCATGTGAAATAAACGACAATTATATATACCTTTTCGTC---	793
CYP52A5A	873	A--TAAATTTGCCACCTCCATCATCAACACAG--CCGCCACTAACTACATCACTCCCTATTTT-----	933
CYP52A5B	936	A--TAAATTTGTCACTTGTGCTGCTTGTCCAC-----CCACAGCATTTCTC-----	978
CYP52A8A	245	-----ACCTGTCAACCCCCCCCCCCCCCCC--CCACTGCC--CTACCCCTGCCCTGC-----	293
CYP52A8B	823	-----ACCTGTCAACCCCCCTCAC-----TGCCCTGCCCTGC-----	853
CYP52D4A	538	CTCCGGTGGTGACAACTTGACACAAAGCAGTTCCGAGAACCCACCAACAATCACCATTCCAG-----	601
*			
CYP52A1A	1017	TTCCCTCACAATTATATAAACTCACCACCATTTCCACAGACCCGTAATTTTCATGTCTCAC-TTCTCTTTT	1085
CYP52A2A	1051	-----CACCAAGACGCAATGAAACGCACATGGACATTTAGACCTCCCCACATGTGATAGTTTGTCTTAAC	1115
CYP52A2B	901	AACTCCACCAAGACACAAATGAATCGCACATGGACATTTAGACCTCCCCACATGTGAAAGCTTCTCTGGCG	970
CYP52A3A	1035	CCTCCTCCTATATCTCTTTTGTCTAC-ATTTGTGTTTTCACGTTTCTTGCTTTTGCACTCTCCCACTCCC	1103
CYP52A3B	794	TGTCCTCCAATGTCTCTTTTGTGCTGCCATTTTGTCTTTTGTCTTTTGTCTTTTGCACTCTCTCCCACTCCC	863
CYP52A5A	934	CTCTCTCTCTCTTTGTCTTACTCCGCTCCCGTTTCTCTTATCCAGAAATACACACAACTCATATAAAGAT	1002
CYP52A5B	979	TTTTCTCTCTCTTTGTCTTACTCCGCTCCCTGTTTCTCTTATCCAGAAATACACACAACTCATATAAAGAT	1048
CYP52A8A	294	CCTGCACGTCCTGTGTTTGTGTGTGTCTTTTCCACGCTATAAAGCCCTGGCGTCCGGCCAAAGGTTT	363
CYP52A8B	854	CCTGCACGCCCTGTGTTTGTGTGTGTGGCACTCCACGCTATAAAGCCCTGGCGTACGGCCAAAGGTTT	923
CYP52D4A	602	TATCACTTCTACATGTCAACCTACGATGTAATCTCATCACCATCTAGTTTCTTGGCAATCGTTTATTGTT	671

FIG. 15D-I

CYP52A1A	1086	GCTCTCTTTTACTTAGTCAGGTTTGATAACTTCCTTTTATTATACCCTATCTTATTATTATTATTATTC	1155
CYP52A2A	1116	AGA-----AAAGTATAATAAGAACCCATGCCGTCCCTTTCTTTTCGCCGCTTCAACTTTTTCCTTTTA	1179
CYP52A2B	971	AAAGCAAAAAAAGTATAATAAGGACCCATGCCCTTCCTCTTCCTGGCCGCTTCAACTTTTCTTTTCT	1040
CYP52A3A	1104	ACAA-----AGAAAAAATACTACACTAAGTCGCTCTCTCCATCGTTT	1146
CYP52A3B	864	ACAATCAGTGCAGCAACACACAAAGAAATAAAAAACCTACACTATGTGCTCTTCTCCATCGTTT	933
CYP52A5A	1003	GCA--ACAATTATAAAGATACGCC-----AGGCCACCTTCTTTTCTTCACTTTTGTGACTGC-A	1064
CYP52A5B	1049	ACG--CTAGCCCCAGCTGCTTTCT-----TTTCTTCACTTTTGGTGCTGCTTTTGGCTGC-T	1110
CYP52A8A	364	TCCACCCAGCCAAAAAACAGCTCTAAAAAATTGGTTGATCCCTTTTGGTTGCAAGGTTT---CCAC-C	429
CYP52A8B	924	TCCTCACAGCCAAAAAA-----AATTGGCTGATCCTTTTGGGCTGCAAGGTTTTCACCCAC-C	982
CYP52D4A	672	ATGGGTCAACATCCAATACAACCTCCACCAA--TGAAGAAGAAAAACGGAAAGCAGAATACCAGAATGACA	739
*			
CYP52A1A	1156	ATTTATACCAACCAACC--AACCATGGCCACACAAGAAATCATCGATTCTGTACTTCCGTACTTGACCAA	1223
CYP52A2A	1180	TCCTT-----ACACACATCAGACCA-TGACTGTACACGATATTATCGCCACATACATTCAACCAA	1236
CYP52A2B	1041	TTGTCTATCAACACACACACACCTCAGACCA-TGACTGCACAGGATATTATCGCCACATACATCACCAA	1109
CYP52A3A	1147	GCCC-----AAGAGGTTCTCGCTACCACTAGTCCTTACATCGAGTACTTTCTTGACA-ACTACACCAAG	1208
CYP52A3B	934	GCTC-----AGGAGGTTCTCGCTACCACTAGTCCTTACATCGAGTACTTTCTTGACA-ACTACACCAAG	995
CYP52A5A	1065	ACTTCTACAATCCACACAGCCACCAAGCCGCTATGATTGAACAACTCCTAGAATATT-----	1127
CYP52A5B	1111	ACTTCTACAACC-----ACCACCAACCAACCAACCATGATTGAACAAATCCTAGAATATT-----	1166
CYP52A8A	430	ACCACCTCCACCA--CCTCAACTATTGAAACAA--AAGATGCTCGATCAGATCTTACATTACT-----	488
CYP52A8B	983	ACCACCAACCA--CCTCAACTATTCAACAA--AGGATGCTCGACCAAGATCTTCCATTACT-----	1041
CYP52D4A	740	GTGTG----AGTTCCTGACCATTGCTAATCTA-TGGCTATATCTAGTTTGTCTATCGTGGGATG-----	797
*			

FIG. 15D-2

CYP52A1A	1224	ATGGTACACTGTGATTACTGCAGCAGTATTAGTCTTCCTTATCTCCACAAACATCAAGAACTACGTCAAG	1293
CYP52A2A	1237	ATGGTACGTGATAGTACCACCTCGCTTTGATTGCTTATAGAGTCTCGACTACTTCTATGGCAGATACTTG	1306
CYP52A2B	1110	ATGGTACGTGATAGTACCACCTCGCTTTGATTGCTTATAGGGTCCCTCGACTACTTTTACGGCAGATACTTG	1179
CYP52A3A	1209	ATGGTACTACTTCATACCTTTGGTGCTTCTTTGTTGAACTTTATAAGTTTGCTCCACACAAGGTACTTG	1278
CYP52A3B	996	ATGGTACTACTTCATACCTTTGGTGCTTCTTTGTTGAACTTTATCATCAGCTTGCTCCACACAAAAGTACTTG	1065
CYP52A5A	1128	--GGTATGTCGTTGTGCCAGTGTGTACATCATCAAACTCACTTGCATACACAAAGACTCGCGTCTTG	1195
CYP52A5B	1167	--GGTATATTGTTGTGCCCTGTGTGTACATCATCAAACTCACTTGCCTACAGCAAGACTCGCGTCTTG	1234
CYP52A8A	489	--GGTACATTGTCTTGCCATTGTTGGCCATTATCAACCAGATCGTGGCTCATGTCAGGACCAATTATTG	556
CYP52A8B	1042	--GGTACATTGTCTTGCCATTGTTGGTCATTATCAAGCAGATCGTGGCTCATGCCAGGACCAATTATTG	1109
CYP52D4A	798	-TGATCTGTGTCGTCCTTCAATTTGCGTTTGTGTTTATTTCGGGTAT-GAATATTGTTATACATAAATACTTG	865

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FIG. 15D-3

CYP52A1A	1294	GCAAAGAAATTGAAATGTGTGATCCACCATACTTGAAGGATGCCCGTCTCAGTGGTATTCTGTCTTTGA	1363
CYP52A2A	1307	ATGTACAAGCTTGGTGCTAAACCATTTTCCAGAAACAGACAGCGGTGTTTCGGATTCAAGCTCCGC	1376
CYP52A2B	1180	ATGTACAAGCTTGGTGCTAAACCGTTTTCAGAAACAAACAGACGGTTATTTCCGGATTCAAGCTCCAC	1249
CYP52A3A	1279	GAACGAGGTTCCACGCCAAGCCACTCGGTAACTTTGTCAAGGACCCCTACGTTTGGTATCGCTACTCCGT	1348
CYP52A3B	1066	GAACGAGGTTCCACGCCAAGCCGCTCGGTAACTCGTGTGGATCCTACGTTTGGTATCGCTACTCCGT	1135
CYP52A5A	1196	ATGAAAAGTTGGTGCTGCTCCAGTCACAAACAAAGTTGTACGACAACGTTTCCGGTATCGTCAATGGAT	1265
CYP52A5B	1235	ATGAAACAGTTGGGTGCTGCTCCAATCACAAACAGTTGTACGACAACGTTTTCGGTATCGTCAACGGAT	1304
CYP52A8A	557	ATGAAGAAATTGGGTGCTAAGCCATTCAACACGTCACCGGTGGTGGCTTCAAAATTGGGCC	626
CYP52A8B	1110	ATGAAGAAATTGGGCGCTAAGCCATTCAACATGTCCAACCTAGACGGGTGGTTTGGCTTCAAAATTGGGCC	1179
CYP52D4A	866	ATGCACAAACATGGCGCTCGAGAAATCGAGAAATGTGATCAACGATGGGTCTTTGGGTTCCGCTTACCTT	935

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CYP52A1A	1364	TCGCCGCCATCAAGGCCAAGAACGACGGTAG-ATTGGCTAACTTTGCC-----GATGAAGTTT	1421
CYP52A2A	1377	TTGAATTGTTGAAGAAAGAGAGCGGCTAC-CCTCATAGACTTCACA-----CTCCAGCGTATC---C	1436
CYP52A2B	1250	TTGAATTGTTAAAGAAAGAGAGTGACGGTAC-CCTCATAGACTTCACT-----CTCGAGCGTATC---C	1309
CYP52A3A	1349	TGCTTTTGATCTACTTGAAGTCGAAAGGTAC-GGTCAATGAAGTTTGCTTGGGCGCTCTGGAAACAACAAGT	1417
CYP52A3B	1136	TGATCTTGATCTACTTAAAGTCGAAAGGTAC-AGTCATGAAGTTTGCCTGGAGCTTCTGGAAACAACAAGT	1204
CYP52A5A	1266	GGAAGGCTCTCCAGTTCAAGAAAGAGGGCAGGGCTCAAGAGTACAACG-----ATTACAAGTTTG---	1325
CYP52A5B	1305	GGAAGGCTCTCCAGTTCAAGAAAGAGGGCAGAGCTCAAGAGTACAACG-----ATCACAAGTTTG---	1364
CYP52A8A	627	GTGAATTCTCCTCAAGCAAAAGTGTGGGAG-CTGGTTGATTAAATC-----ATCTCCCGTTT-----	684
CYP52A8B	1180	GTGAATTCTCCTCAAGCTAAAGTGTGGGAG-GCAGGTTGATTAAATC-----ATCTCCCGTTT-----	1237
CYP52D4A	936	TGCTACTCATCGGAGCCAGCAATGAGGCGG-ACCTATCGAGTTCAAGT-----GTCAAGAGATTCGAGT	998

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FIG. 15E-1

CYP52A1A	1422	----	CGACGAGTACCCAAACACACCTTCTACTTGTCTGTGTGCCGGTGCTTTGAAGATTGTGCTGACTGT	1487
CYP52A2A	1437	ACGATCTCGATCGTCCCGATATCCCAACTTTTCACATTC	CCCGGTCTTTTCCATCAACCTTGTCAATACCCCT	1506
CYP52A2B	1310	AAGCGTCAATCGTCCAGATATCCCAACTTTTACATTTCCCAATCTTTTCCATCAACCTTATCAGCACCCCT		1379
CYP52A3A	1418	ACATCGTCAGAGACCCAAAGTACAAAGACAACCTGGGCTCAGGATTGTTGGCCTCCCATTTGATTGAAACCAT		1487
CYP52A3B	1205	ACATTGTCAAAGACCCAAAGTACAAAGACCACCTGGCCTTAGAATTGTCGGCCTCCCATTTGATTGAAACCAT		1274
CYP52A5A	1326	ACCACTCCAAGAACCCCAAGCGTGGGCACCTACGTCAGTATTCTTTTCGGCACCCAGGATCGTCGTGACCAA		1395
CYP52A5B	1365	ACAGCTCCAAGAACCCCAAGCGTCGGCACCTATGTGAGTATTCTTTTGGCACCAAGATTGTCGTGACCAA		1434
CYP52A8A	685	-----CCACGA----	TAATGAGGACACTTCTCCAGCTATGCTTTTGGCAACCATGTGGTGTTCACCCAG	744
CYP52A8B	1238	-----CCACGA----	TAATGAGGACACTTCTCCAGCTATGCTTTTGGCAACCATGTGGTGTTCACCCAG	1297
CYP52D4A	999	-CGGCGCCACAT--CCACAGAACAGACATTTGGTCAACCGGGCATTGAGCGTTTCTGTGATACTCACCCAA		1065
		*	* * *	**
CYP52A1A	1488	TGACCCAGAAAAACATCAAGGCTGTCTTTGGCCACCCAAATTCACTGACTTCTCTCTGGGTACCAGACACGCC		1557
CYP52A2A	1507	TGAGCCGGAGAACATCAAGGCCATCTTTGGCCACTCAGTTCAACGATTCTCTCTGGGTACCAGACACTCG		1576
CYP52A2B	1380	TGAGCCGGAGAACATCAAGGCTATCTTTGGCCACCCAGTTCAACGATTCTCTCTGGGTACCAGACACTCG		1449
CYP52A3A	1488	GGACCCAGAGAACATCAAGGCTGTTTTGGCTACTCAGTTCAATGATTTCTCTTTGGGAACCCAGACACGAT		1557
CYP52A3B	1275	AGACCCAGAGAACATCAAAAGCTGTGTGGCTACTCAGTTCAACGATTTCTCTCTGGGAACCTAGACACGAT		1344
CYP52A5A	1396	AGATCCAGAGAAATATCAAAAGCTATTTTGGCAACCCAGTTTGGTGATTTTTCTTTGGCAAGAGGCACACT		1465
CYP52A5B	1435	GGATCCAGAGAAATATCAAAAGCTATTTTGGCAACCCAGTTTGGCGATTTTTCTTTGGCAAGAGACACGCT		1504
CYP52A8A	745	GGACCCCGAGAAATATCAAGGCGCTTTTGGCAACCCAGTTTGGTGATTTTTCTTTGGCAGCAGGGTCAAG		814
CYP52A8B	1298	GGACCCCGAGAAATATCAAGGCGCTTTTGGCAACCCAGTTTGGTGATTTTTCTTTGGGAAGCAGGGTCAAA		1367
CYP52D4A	1066	GGACCCAGTGAATATCAAAAGCGATGCTATCGACCCAGTTTGTGATGACTTTTCCCTTGGGTGAGACTACAC		1135
		** * * *	** * * *	**

FIG. 15E-2

CYP52A1A	1558	CAC	T	T	G	C	C	T	T	G	T	G	G	T	G	A	C	G	G	T	A	T	C	T	T	C	A	C	C	T	T	G	A	C	G	G	A	A	G	G	T	T	G	A	A	G	C	A	C	T	C	C	A	G	A	G	C	T		
CYP52A2A	1577	CAC	T	T	G	C	T	C	T	T	G	T	G	G	T	G	A	T	G	T	A	T	C	T	T	A	C	G	T	T	G	A	C	G	C	C	G	G	T	T	G	A	A	G	C	A	C	A	G	A	T	C	T	A						
CYP52A2B	1450	CAC	T	T	G	C	T	C	T	T	G	T	G	G	C	A	T	G	T	A	T	C	T	T	A	C	T	T	G	A	C	G	T	G	C	C	G	G	T	T	G	A	A	G	C	A	C	A	G	A	T	C	T	A						
CYP52A3A	1558	T	T	C	T	T	G	T	A	C	T	T	G	T	G	G	T	A	C	C	T	T	T	C	A	C	C	T	T	G	A	C	G	T	G	C	T	G	G	T	T	G	A	A	A	C	A	T	A	G	A	A	C	T	A					
CYP52A3B	1345	T	T	C	T	T	G	T	A	C	T	T	G	T	G	G	C	A	T	G	T	A	T	T	T	T	A	C	C	T	T	G	A	C	G	T	G	C	T	G	G	T	T	G	A	A	C	A	C	A	G	T	A	A	C	T	A			
CYP52A5A	1466	C	T	T	T	T	A	A	G	C	C	T	T	T	G	T	A	G	G	T	A	T	C	C	A	T	T	T	G	A	C	G	G	C	A	A	G	G	T	T	G	A	A	G	C	A	C	A	G	A	G	C	C	A						
CYP52A5B	1505	C	T	T	T	T	A	A	A	C	C	T	T	T	G	T	A	G	G	T	A	T	C	C	A	C	C	T	T	G	A	C	G	G	C	A	A	G	G	T	T	G	A	A	G	C	A	T	A	G	C	A	G	A	T	C	C	A		
CYP52A8A	815	T	T	C	T	T	C	A	A	A	C	C	A	T	A	T	T	G	G	G	T	A	C	C	T	T	C	A	T	T	G	A	C	G	C	C	A	A	G	G	T	T	G	A	A	G	C	A	C	A	G	A	G	C	C	A				
CYP52A8B	1368	T	T	C	T	T	C	A	A	A	C	C	A	T	T	G	T	G	G	G	T	A	C	C	T	T	C	A	C	C	T	T	G	A	C	G	C	G	A	A	G	G	T	T	G	A	A	G	C	A	C	A	G	A	G	C	C	A		
CYP52D4A	1136	C	A	G	T	T	G	C	C	C	G	T	T	G	T	T	G	G	G	A	A	G	G	C	A	T	C	T	T	T	G	A	C	G	C	C	C	A	G	A	G	T	T	G	A	A	G	C	A	G	A	G	C	C	G	A	T	C	T	A

**FIG. 15E-3**



CYP52A1A	1628	TGTTGAGACCA	CAGTTTGCTAGAGACCAGATTGGACACAGTTAAAGCCTTGGAAACCA	CACATCCAAATCAT	1697
CYP52A2A	1647	TGTTGAGACCA	CAGTTTGCCAGAGAACAGATTTCACAGTCAAGTTGTTGGAGCCA	CACAGTTTACGGTGT	1716
CYP52A2B	1520	TGTTGAGACCA	CAGTTTGCCAGAGAACAGATTTCACAGTCAAGTTGTTGGAGCCA	CACATGCAGGTGT	1589
CYP52A3A	1628	TGTTGAGACCA	CAGTTTGCTAGAGAACAGTTTCTCAGTCAAGTTGTTGGAGCCA	CACAGTTTACGGTGT	1697
CYP52A3B	1415	TGTTGAGACCA	CAGTTTGCTAGAGAACAGTTTCCACGTCAAGTTGTTGGAAACCA	CACAGTTTACGGTGT	1484
CYP52A5A	1536	TGTTGAGACCA	CAGTTTGCCAGAGAACAGTTGCTCATGTGACGTGCTGTTGGAAACCA	CACAGTTTCCAGTTGT	1605
CYP52A5B	1575	TGTTGAGACCA	CAGTTTGCCAGAGAACAGTTGCTCATGTGACGTGCTGTTGGAAACCA	CACATTCAGTTGT	1644
CYP52A8A	885	TGTTGAGACCA	CAGTTTGCCAGAGAACAGTTGCTCATGTGACGTGCTGTTGGAAACCA	CACATTCAGTTGT	954
CYP52A8B	1438	TGTTGAGACCA	CAGTTTGCCAGAGAACAGTTGCTCATGTGACGTGCTGTTGGAAACCA	CACATTCAGTTGT	1507
CYP52D4A	1206	TGTTGCGTCCG	CAATTGCGCAATTTGCCAAAGATCGGGTTTCTCATATCCTGGATCTAGAACCGCA	TTTGTGTGCT	1275
		****	* ** * * * * *	* ** * *	*
CYP52A1A	1698	GGCTAAGCAGAT	CAAGTTGAACCAAGGAAAGACTTTCGATATCCAAGAA	TTGTTCTTTAGATTACCGTC	1767
CYP52A2A	1717	CTTCAAAACAC	GTGAGAAAGGCACAGGGCAAGACTTTTGACATCCAGGAA	TTGTTTTCAGATTGACCGTC	1786
CYP52A2B	1590	CTTCAAGCAC	GTGAGAAAGGCACAGGGCAAGACTTTTGACATCCCAAGAA	TTGTTTTCAGATTGACCGTC	1659
CYP52A3A	1698	CTTCAAGCAC	GTGAGAAAGGCACCGCGGTCAAAAGTTTCGACATCCAAGAA	TTGTTCTTCAGGTTGACCGTC	1767
CYP52A3B	1485	CTTCAAGCAC	GTGAGAAACACCGCGGTGAGACTTTTGACATCCCAAGAA	TTGTTCTTCAGATTGACCGTC	1554
CYP52A5A	1606	GAAGAAAGCAT	ATTCTTTAAGCACAAAGGTGAATACTTTGATATCCAGGAA	TTGTTCTTTAGATTACCGTT	1675
CYP52A5B	1645	GAAGAAAGCAT	ATTCTTTAAGCACAAAGGTGAGTACTTTGATATCCAGGAA	TTGTTCTTTAGATTACCGTC	1714
CYP52A8A	955	GAAGAAAGCAT	ATTCTTTAAGCACAAAGGTGAATACTTTGATATCCAGGAA	TTGTTCTTTAGATTACCGTC	1024
CYP52A8B	1508	GAAGAAAGCAT	ATTCTTTAAGCACAAAGGTGAATACTTTGATATCCAGGAA	TTGTTCTTTAGATTACCGTT	1577
CYP52D4A	1276	TCGGAAGCACAT	TGATGGCCACAATGGAGACTACTTCGACATCCAGGAGCTCTACTTCCGGT	TCTCTCGATG	1345
		** ** *	** * * * * *	* ** * *	*

FIG. 15F-1

CYP52A1A	1768	GACACCGCTACTGAGTCTTGTGTTGGTGAATCCGTTCACTCCTTGACGATGAAAAATTGGGCATCCCAA	1837
CYP52A2A	1787	GACTCCGCCACCGAGTTTTTGTGTTGGTGAATCCGTTGAGTCCCTTGAGAGATGAATCTATCGGCATGTCCA	1856
CYP52A2B	1660	GACTCCGCCACTGAGTTTTTGTGTTGGTGAATCCGTTGAGTCCCTTGAGAGATGAATCTATTTGGGATGTCCA	1729
CYP52A3A	1768	GACTCCGCCACCAGATTCTTGTGTTGGTGAATCCCTGCTGAATCCCTTGAGGGACGAATCTATTTGGAATTGACCC	1837
CYP52A3B	1555	GACTCCGCCACCAGATTCTTGTGTTGGTGAATCCCTGCTGAATCCCTTGAGAGACGACTCTGTTGGTTTGACCC	1624
CYP52A5A	1676	GATTCGGCCACCGGAGTTCTTATTTGGTGAGTCCGTCACCTCTTAAAGGACGAATCTATTTGGTATCAACC	1745
CYP52A5B	1715	GACTCGGCCACGGAGTTCTTATTTGGTGAGTCCGTCACCTCTTAAAGGACGAATCTATCGGTATCAACC	1784
CYP52A8A	1025	GACTCGGCCACGGAGTTCTTATTTGGTGAGTCCGTCACCTCTTAAAGGACGAGGAAATTTGGCTACGACA	1094
CYP52A8B	1578	GATTCAGCGACGGAGTTCTTATTTGGTGAGTCCGTCACCTCTTAAAGGACGAGGAAATTTGGCTACGATA	1647
CYP52D4A	1346	GATGTGGCGACGGGTTTTTGTGTTGGCGAGTCTGTGGGTCGTTGAAAGACGAAAGATGCGAGG-----	1408
		** ** ** * ** * ** * ** * ** * ** *	
CYP52A1A	1838	CTCCAAACGAAA---TCCCAGGAAGAGAAAACTTTGCCGCTGCTTTCAACGTTTCCCAACACTACTTGGC	1904
CYP52A2A	1857	TCAATGCGCTTGACTTTGACGGCAAGCTGGCTTTGCTGATGCTTTTAACTATTTCGCAGAAATTAATTGGC	1926
CYP52A2B	1730	TCAATGCACCTTGACTTTGACGGCAAGCTGGCTTTGCTGATGCTTTTAACTACTCGCAGAACTATTGGC	1799
CYP52A3A	1838	CAACCAACCAAGGATTTTCGATGGCAGAAGAGATTTTCGCTGACGCTTTCAACTATTTCGCAGACTTACCAGGC	1907
CYP52A3B	1625	CAACCAACCAAGGATTTTCGAAAGCAGAGAGATTTTCGCTGACGCTTTCAACTACTTCGCAGACTTACCAGGC	1694
CYP52A5A	1746	AAGACGATATAGATTTTGTCTGGTAGAAAGGACTTTTGTGAGTCGTTCAACAAAGCCCAGGAATACTTGGC	1315
CYP52A5B	1785	AAGACGATATAGATTTTGTCTGGTAGAAAGGACTTTTGTGAGTCGTTCAACAAAGCCCAGGAGTATTGTC	1854
CYP52A8A	1095	CGAAAGACATGT---CTGAAGAAAGACGCAGATTTTGGCGACGCGTTCAACAAAGTCGCAAGTCTACGTGGC	1161
CYP52A8B	1648	CGAAGGACATGG---CTGAAGAAAGACGCAGAAATTTTGGCGACGCGTTCAACAAAGTCGCAAGTCTATTGTC	1714
CYP52D4A	1409	-----TTCCTGGAAGCATTCATAGTCGAGAAAGTATTTGGC	1445
		** ** * ** * ** * ** * ** * ** *	

FIG. 15F-2

CYP52A1A	1905	CACCAGAGTTACTCCAGACTTTTACTTTTTGACCAACCTAAGGAATTCAGAGACTGTAAACGCCAAG	1974
CYP52A2A	1927	TTCGAGAGCGGTTATGCAACAATGTACTGGGTGTTGAACGGGAAAAAGTTTAAAGGAGTGCAACGCTAAA	1996
CYP52A2B	1800	TTGAGAGCGGTTATGCAACAATGTACTGGGTGTTGAACGGGAAAAAGTTTAAAGGAGTGCAACGCTAAA	1869
CYP52A3A	1908	CTACAGATTTTGTGCAACAATGTACTGGATCTTGAATGGCTCGGAATTCAGAAAGTCGATTGCTGTC	1977
CYP52A3B	1695	CTACAGATTTTGTGCAACAATGTACTGGATTTTGAATGGCGCGGAATTCAGAAAGTCGATTGCCATC	1964
CYP52A5A	1816	TATTAGAACCTTGGTGCAGACGTTCTACTGGTTGGTCAACAACAAGGAGTTTAGAGACTGTACCAAGCTG	1885
CYP52A5B	1855	TATTAGAAATTTGGTGCAGACCTTCTACTGGTTGATCAACAACAAGGAGTTTAGAGACTGTACCAAGCTG	1924
CYP52A8A	1162	CACCAGAGTTGCTTTACAGAACTTGTAAGTTGGTCAACAACAAGAGTTCAAGGAGTGCAATGACATT	1231
CYP52A8B	1715	CACCAGAGTTGCTTTACAGACATTTGTAAGTTGGTCAACAACAAGAGTTCAAGGAGTGCAACGACATT	1784
CYP52D4A	1447	AACTAGGGCAACGTTGCACGAGTTGTACTTTCTTTGTGACGGGTTTAGGTTTCGCCAGTACAAACAGGTT	1516

FIG. 15F-3

CYP52A1A	1975	GTCCACCACTTGGCCCAAGTACTTGTCAACAAGCCCTTGAACTTTACTCTGAAGAACTCGAAGAGAAAT	2044
CYP52A2A	1997	GTGCACAAAGTTTGTGCTACTACTACGTCAACAAGGCTTTGGACTTTGACGCTGAACAAATTGGAAAAGGAGG	2066
CYP52A2B	1870	GTGCACAAAGTTTGTGCTACTACTACGTCAACAAGGCTTTGGACTTTGACACCTGAACAAATTGGAAAAGCAGG	1939
CYP52A3A	1978	GTGCACAAAGTTTGTGCTGACCACTATGTGCAAAAAGGCTTTGGAGTTGACCGACGATGACTTGCAGAAAACAAG	2047
CYP52A3B	1765	GTGCACAAAGTTTGTGCTGACCACTATGTGCAAAAAGGCTTTGGAGTTGACCGACGATGACTTGCAGAAAACAAG	1834
CYP52A5A	1886	GTGCACAAAGTTTACCAACTACTATGTTCAGAAAAGCTTTGGATGCTAGCCCAAGAGAGCTTGAAAAGCAAA	1955
CYP52A5B	1925	GTGCACAAAGTTTACCAACTACTATGTTCAGAAAAGCTTTGGATGCTAGCCCAAGAGAGCTTGAAAAGCAAG	1994
CYP52A8A	1232	GTCCACAAAGTTTACCAACTACTATGTTCAGAAAAGCTTTGGATGCTAGCCCAAGAGAGCTTGAAAAGCAAG	1301
CYP52A8B	1785	GTCCACAAAGTTTACCAACTACTATGTTCAGAAAAGCTTTGGATGCTAGCCCAAGAGAGCTTGAAAAGCAAG	1854
CYP52D4A	1517	GTGCGAAAGTTCTGCAGCCAGTGTGCCACAAGGCTTAGATGTTGCACCGGAAGACACC-----A	1577
		** * * * * * * * * * * *	
CYP52A1A	2045	CCAAAGTCCGGTTACGTTTCTTGTACGAATTGGTTAAGCAAAACCAGAGATCCAAAAGGCTTGAAGATCA	2114
CYP52A2A	2067	ATGGTT-----ATGTGTTTTTGTACGAATTGGTCAAGCAAAACCAGAGACAAGCAAGTGTGTGAGAGACCA	2130
CYP52A2B	1940	ATGGTT-----ATGTGTTCTTGTACGAGTTGGTCAAGCAAAACCAGAGACAGGCAAGTGTGTGAGAGACCA	2003
CYP52A3A	2048	ACGGCT-----ATGTGTTCTTGTACGAGTTGGTCAAGCAAAACCAGAGACCCCAAGGCTTGTGAGAGACCA	2111
CYP52A3B	1835	ACGGCT-----ATGTGTTCTTGTACGAGTTGGTCAAGCAAAACCAGAGACCCCAAGGCTTGTGAGAGACCA	1898
CYP52A5A	1956	GTGGGT-----ATGTGTTCTTGTACGAGCTTGTCAAGCAGACAAGAGACCCCAATGTGTTCGTGACCA	2019
CYP52A5B	1995	GCGGGT-----ATGTGTTCTTGTATGAGCTTGTCAAGCAGACGAGAGACCCCAAGGTTGTTCGTGACCA	2058
CYP52A8A	1302	GCGGGT-----ATGTGTTCTTGTATGAGCTTGTCAAGCAGACGAGAGACCCCAAGGTTGTTCGTGACCA	1365
CYP52A8B	1855	GCGGGT-----ATGTGTTCTTGTACGAGCTTGTCAAGCAGACGAGAGACCCCAAGGTTGTTCGTGACCA	1918
CYP52D4A	1578	GCGAGT-----ACGTGTTTCTCCGGAGTTGGTCAACACACTCGAGATCCCGTTGTTTACAAAGACCA	1641
		* * * * * * * * * * * *	

FIG. 15G-I

CYP52A1A	2115	ATTGTTGAACATTATGTTGCCGGAAGAGACACCACTGCCGGTTTGTGTCTCTTTCCTTTGTTGAATTG	2184
CYP52A2A	2131	ATTGTTGAACATCATGTTGCTGTTAGAGACACCAACCCCGCGTTTGTGTCTCTTTCCTTTGAATTG	2200
CYP52A2B	2004	GTTGTTGAACATCATGTTGCCGGTAGAGACACCAACCCCGCGTTTGTGTCTCTTTCCTTTGAATTG	2073
CYP52A3A	2112	GTTATTGAACATTTTGTGTTGCCGGTAGAGACACCAACCCCGCGTTTGTGTCTCTTTCCTTTGAATTG	2181
CYP52A3B	1899	GTTGTTGAACATTTTGTGTTGCCGGTAGAGACACCAACCCCGCGTTTGTGTCTCTTTCCTTTGAATTG	1968
CYP52A5A	2020	GTCCTTGAACATCTTGTGTTGCCGGTAGAGACACCACTGCTGGGTTGTGTCTCTTTCCTTTGAATTG	2089
CYP52A2B	2059	GTCCTTGAACATCTTGTGTTGCCGGTAGAGACACCACTGCTGGGTTGTGTCTCTTTCCTTTGAATTG	2128
CYP52A8A	1366	GTCCTTGAACATCTTGTGTTGCCGGTAGAGACACCACTGCTGGGTTGTGTCTCTTTCCTTTGAATTG	1435
CYP52A8B	1919	GTCCTTGAACATCTTGTGTTGCCGGTAGAGACACCACTGCTGGGTTGTGTCTCTTTCCTTTGAATTG	1998
CYP52D4A	1642	AGCGTTGAACGTCCTTGTGTTGGACGCGACACCAACCCCGTCGTTATTATCGTTTGCAACATTTGAGCTA	1711
		***** *	
CYP52A1A	2185	GCTAGACACCCAGAGATGTGGTCCAAGTTGAGAGAAGAAATCGAAGTTAACTTTGGTGTGGTGAAGACT	2254
CYP52A2A	2201	GCCAGAAACCCAGAAAGTTACCAACAAGTTGAGAGAAGAAATGAGGACAAAGTTTGGACTCGGTGAGAAATG	2270
CYP52A2B	2074	GCCAGAAACCCAGAGGTGACCAACAAGTTGAGAGAAGAAATCGAGGACAAAGTTTGGTCTTGGTGAGAAATG	2143
CYP52A3A	2182	TCAAGAAACCCCTGAGGTGTTTGCTAAGTTGAGAGAGGAGTGGAACAAACAGATTGGACTCGGTGAAGAAG	2251
CYP52A3B	1969	TCGAGAAACCCCTGAAGTGTTCGCAAGTTGAGAGAGGAGTGGAACAAACAGATTGGACTCGGCGAAGAGG	2038
CYP52A5A	2090	GCCAGACACCCAGAGATCTGGGCCAAGTTGAGAGAGGAAATGAAACAAACAGTTTGGTCTTGGAGAAGACT	2159
CYP52A5B	2129	GCCAGAAACCCACACATCTGGGCCAAGTTGAGAGAGGAAATGAAACAGCAGTTTGGTCTTGGAGAAGACT	2198
CYP52A8A	1436	GCCAGAAACCCACACATCTGGGCCAAGTTGAGAGAGGAAATGAAACAGCAGTTTGGTCTTGGAGAAGACT	1505
CYP52A8B	1989	GCCAGGAAACCCACACATCTGGGCCAAGTTGAGAGAGGAAATGAAATCAGCTTTGGCTGGGTGAGGACT	2058
CYP52D4A	1712	GCCCAGGAATGACCACATGTGGAGGAAGCTACGAGGAGGTT-----ATCCTGA---CGATGGGACCG	1771
		* *	

FIG. 15G-2

CYP52A1A	2255	CCCGCGTTGAAGAAATTACCTTCGAAGCCCTTGAAGAGATGTGAATACTTGAAGGCTATCCTTAACGAAAC	2324
CYP52A2A	2271	CTAGTGTGTAAGACATTTCCCTTTGAGTCGTTGAAGTCCTGTGAATACCTTGAAGGCTGTTCTCAACGAAAC	2340
CYP52A2B	2144	CTCGTGTGTAAGACATTTCCCTTTGAGTCGTTGAAGTCATGTGAATACCTTGAAGGCTGTTCTCAACGAAAC	2213
CYP52A3A	2252	CTCGTGTGTAAGAGATCTCGTTTGAGTCCTTTGAAGTCTTGTGAGTACTTGAAGGCTGTCAATCAATGAAAC	2321
CYP52A3B	2039	CTCGTGTGTAAGAGATCTCTTTTGAGTCCTTTGAAGTCTCTGTGAGTACTTGAAGGCTGTCAATCAATGAAAGC	2108
CYP52A5A	2160	CTCGTGTGTAAGAGATTACCTTTGAGAGCTTGAAGAGATGTGAGTACTTGAAGGCTTCCCTTAATGAAAC	2229
CYP52A5B	2199	CTCGTGTGTAAGAGATTACCTTTGAGAGCTTGAAGAGATGTGAGTACTTGAAGGCTTCCCTTAACGAAAC	2268
CYP52A8A	1506	CTCGTGTGTAAGAGATTACCTTTGAGAGCTTGAAGAGATGTGAGTACTTGAAGGCTGTTGAACGAAAC	1575
CYP52A8B	2059	CTCGTGTGTAAGAGATTACCTTTGAGAGCTTGAAGAGATGTGAGTACTTGAAGGCTGTTGAACGAAAC	2128
CYP52D4A	1772	TCCAG--TGATGAAATAACCGTGGCCGGTTGAAGAGTTGCCGTTACCTCAAAGCAATCCTAAACGAAAC	1839

FIG. 15G-3

CYP52A1A	2325	CTTGGTATGTACCCATCTGTCTCTCAACTTTAGAAACCGCCACCCAGAGACACCACTTTGGCCAAGAGGT	2394
CYP52A2A	2341	CTTGAGATTGTACCCATCCGTGCCACAGAAATTTAGAGTTGCCACCAAGAACACTACCCCTCCCAAGAGGT	2410
-CYP52A2B	2214	TTTGAGATTGTACCCATCCGTGCCACAGAAATTTAGAGTTGCCACCAAAAAACACTACCCCTTCCAAGGGGA	2283
CYP52A3A	2322	CTTGAGATTGTACCCATCCGTGCCACACAACTTTAGAGTTGCTACCCAGAAAACACTACCCCTCCCAAGAGGT	2391
CYP52A3B	2109	CTTGAGATTGTACCCATCTGTTCCACACAACTTCAGAGTTGCCACCCAGAAAACACTACCCCTTCCAAGAGGC	2178
CYP52A5A	2230	CTTGCGTATTTACCCAAAGTGTCCCAAGAAACTTCAGAAATCGCCACCAAGAACACGACATTTGCCAAGGGGC	2299
CYP52A5B	2269	CTTGCGTGTTTACCCAAAGTGTCCCAAGAAACTTCAGAAATCGCCACCAAGAAATACAACTTTGCCAAGGGGT	2338
CYP52A8A	1576	TTTGAGATTACACCCCAAGTGTCCCAAGAAACGCAAGATTTGCGATTAAAGACACGACTTTACCAAGAGGC	1645
CYP52A8B	2129	GTTGAGATTACACCCCAAGTGTCCCAAGAAACGCAAGATTTGCGATTAAAGACACGACTTTACCAAGAGGC	2198
CYP52D4A	1840	TCTTCGACTATACCCCAAGTGTGCTAGGAAACGCGAGATTTTGCTACGAGGAATACGACGCTTCCCTCGTGGC	1909
		* * * * *	* * * * *
CYP52A1A	2395	GGTGGTGCTAACGGGTACCGACCCCAATCTACATTCCTAAAGGCTCCACTGTTGCTTACGTTGTCTACAAGA	2464
CYP52A2A	2411	GGTGGTAAGGACGGGTGTCTCCTGTTTGGTGAGAAAGGGTCAGACCGTTATTACGGTGTCTACGCAG	2480
CYP52A2B	2284	GGTGGTAAGGACGGGTATCTCCTGTTTGGTCAGAAAGGGTCAAAACCGTTATGTACGGTGTCTACGCTG	2353
CYP52A3A	2392	GGTGGTGAAGATGGATACTCGCCAAATTTGTCGTCAAGAAAGGGTCAAGTTGTCTATGACACTGTTATTGCTA	2461
CYP52A3B	2179	GGTGGTAAAGACGGGATGCTCGCCAAATTTGTGTCAAGAAAGGGTCAAGTTGTCTATGTACACTGTCAATTGGTA	2248
CYP52A5A	2300	GGTGGTTCAGACGGTACCTCGCCAAATCTTGATCCAAAAGGGAGAAAGCTGTGTCGTATGGTATCAACTCTA	2369
CYP52A5B	2339	GGTGGTCCAGACGGTACCCAGCCAAATCTTGATCCAAAAGGGAGAAAGGTGTGTCGTATGGTATCAACTCTA	2408
CYP52A8A	1646	GGTGGCCCCAACGGCAAGGATCCCTATCTTGATCAGGAAAGGATGAGGTGGTGCAGTACTCCATCTCGGCAA	1715
CYP52A8B	2199	GGTGGCCCCAACGGCAAGGATCCCTATCTTGATCAGAAAGAAATGAGGTGGTGCATACTCCATCTCGGCAA	2268
CYP52D4A	1910	GGAGGTCCAGATGGATCGTTTCCGATTTTGATAAGAAAGGGCCAGCCAGTGGGTATTTTCATTTGTGCTA	1979
		** ** *	** ** *

FIG. 15H-I

**FIG. 15H-2**



CYP52A1A	2605	GCCTTGACTGAAGCTTCTTATGTGATCACTAGATTGGCCCCAGATGTTTGAAACTGTCTCATCTGATCCAG	2674
CYP52A2A	2621	GCCTTGACAGAAAGCTTCGTATGTCACTGTCAAGTTGCTCCAGGAGTTTGACACACTTGTCTATGGACCCAG	2690
CYP52A2B	2494	GCCTTGACAGAAAGCTTCGTATGTCACTGTCAAGTTGCTCCAGGAGTTTGACACACTTGTCTATGGACCCCA	2563
CYP52A3A	2602	GCCTTGACCGAAAGCTTCATACGTCACTGTCAAGTTGCTCCAGGAGTTTGACACACTTGTCTATGGACCCAG	2671
CYP52A3B	2389	GCCTTGACTGAAGCTTCATACGTCACTGTCAAGTTGCTCCAGGAGTTTGACACACTTGTCTCCCTGGATCCAA	2458
CYP52A5A	2510	GCCTTGACGGAAGCTGGCTATGTGTTGGTTAGATTGGTGCAAGAGTTCTCCACGTTAGGCTGGACCCAG	2579
CYP52A5B	2549	GCCTTGACCGAAAGCTGGTTACGTTTGGTCAAGTTGGTGCAAGAGTTCTCCACATTAGGCTGGACCCAG	2618
CYP52A8A	1856	GCTTTGACTGAAGCCGGTTACGTTTGGTTAGACTTGTTCAGGAGTTTCCAAAATTGTGTCAAGACCCCG	1925
CYP52A8B	2409	GCTTTGACCGAAAGCCGGTTACGTTTGGTTAGACTTGTTCAGGAAATTCCTTAGCTTGTACAGGACCCCG	2478
CYP52D4A	2120	GCAATCCTTGAAAGCTTCGTATGTTTGGCTCGATTGACACACAGTGCTACACGACGATACAGCTTAG--AA	2186

FIG. 15H-3

CYP52A1A	2675	GTCTCGAATA	CCCTCCACCAAAGTGTATTCACTTGACCATGAGTCACAAACGATGGTGTCTCTTTGTCAAGAT	2744
CYP52A2A	2691	ACACCGAATAT	CCACCTAAGAAAAATGTGCGATTTGACCATGTGCTTTTCGACGGTGCCAAATATTGAGAT	2760
CYP52A2B	2564	ACACCGAATAT	CCACCTAGGAAAAATGTGCGATTTGACCATGTCCCTTTTCGACGGTGCCAAACATTTGAGAT	2633
CYP52A3A	2672	ACACCGAATAT	CCACCAAATTTGCAGAACACCTTGACCTTGTGCTCTTTTGATGGTGCTGATGTTAGAAT	2741
CYP52A3B	2459	ACGCTGAGTAC	CCCAACCAAAATTCAGAGAACACCTTGACCTTGTCACTCTTTTGATGGTGCTGACGTTAGAAT	2528
CYP52A5A	2580	ACGAGGTGTAC	CCCGCCAAAGAGGTTGACCAACTTGACCAATGTGTTTGACGGATGGTGCTATTGTCAAAGTT	2649
CYP52A5B	2619	ATGAAGTGTAT	CCACCAAGAGGTTGACCAACTTGACCAATGTGTTTGACGGATGGTGCTATTGTCAAAGTT	2688
CYP52A8A	1926	AAACCAAGTAC	CCACCACTAGATTGGCACACTTGACGATGTGCTTGTGCTTTTGACGGTGACACGTCAAAGAT	1995
CYP52A8B	2479	AAACTGAGTAC	CCCAACCACTAGATTGGCACACTTGACGATGTGCTTGTGTTTGACGGGGCATACGTCAAAGAT	2548
CYP52A8C	2187	CTACCGCACTA	CCCAACCAAACTCGTTCACTCTCAGATGAGTCTTCTCAACGGGGGTGATCATCCGGAAC	2256

[illegible]

CYP52A1A	2745	GTAA-AGTAGTCGATGCTGGGTATTTCGATTACATGT--GTATAGGAAGATTTTGGTTTTTTTATTTCGTTCT	2811
CYP52A2A	2761	GTATTAGAGGGTCATGTGTTATTTT-GATTGTTTA----GTTTGTAATTACTGATTAGGTTAATTCATG	2824
CYP52A2B	2634	GTATTAGAGGATCATGTGTTATTTTGTATTGGTTTAGTCTGTTGTAGCTATTGATTAGGTTAATTCACG	2703
CYP52A3A	2742	GTA <sup>CTAA</sup> GGTTGCTTTTCCCTTGCTAAATTTTCTCTGTATAGCTTGTGTATTTAAATTTGAATCGGCAATTG	2811
CYP52A3B	2529	GTTCTAAAGGTTGCTTATCCTTGCTAGTGTTATT--TATAGTTTGTGTATTTAAATTTGAATCGGCGATTG	2595
CYP52A5A	2650	TGACTAGCGCGTGGTGAATGCGTTTGATTTTGTA--GTTTCTGTTTGCAGTAATGAGATAACTATTCA	2716
CYP52A5B	2689	TGACTAGTA-CGTA-TGAGTGCGTTTGATTTTGTA--GTTTCTGTTTGCAGTAATGAGATAACTATTCA	2753
CYP52A8A	1996	GTCATAGGTTTCCC---CATACAAGTAGTTCAGTA--ATTATACACTGTTTTTACTTTTCTCTCTCATACC	2059
CYP52A8B	2549	GCAATAGGTTT-----TGTTTTGACTTTTGTTTCCATA--	2580
CYP52D4A	2257	TAGAACTTGATTATGTGTTTTATGGTTAATCGGGGCAAGCACTGCAAGTCATTGATGTTTTGTGGAAAGCCC	2326

FIG. 15-1

CYP52A1A	2812	TTTTTTTAAATTTTGTGTTAAATTAG-TTTAGAGATTTCATTAAATACATAGATGGGTGCTATTTCGAAACT	2880
CYP52A2A	2825	GATTGTTATTATTGATAGGGGT - - - - - TCGCGTGTGTCATTCACTTGGGATCGTTCCAGGTTG	2885
CYP52A2B	2704	GATTGTTATTATTGATAGGGGGTGGTGTGTGTGTGTCATTTCACATGGGATCGTTCCAGGTTG	2773
CYP52A3A	2812	ATTTTCTGTATACCAATAAACCGTA - - - - - GTGCGATTGACCAAAACCGTTCAAAAGTTTGTGTTCTC	2873
CYP52A3B	2596	ATTTTCTGTGTACTAATAACTGTA - - - - - GTGGGTTTGTACCAAAACCGTTCAAAAGTTTGTGTTCTC	2657
CYP52A5A	2717	GATAAGGCGAGTGGATGTACGTTT-TGTAAGAGTTT - - - - - CCT-TACAACCTTGGTGGG-TGTGTAGGTT	2781
CYP52A5B	2754	GATAAGGCGGTGGATGTACGTTT-TGTAAGAGTTT - - - - - CCT-TACAACCTTGGTGGG-TGTGTAGGTT	2817
CYP52A8A	2060	AAATGGACAAAAGTTTAAAGCATG-CCTAACACGTGACCG-GACAATTGTGTGCGCACTAGTATGTAACA	2127
CYP52A8B	2581	- - - - - TGC AAGT	2587
CYP52D4A	2327	AGCATTGGTGTTCGGAGCATCAATAACCAATGTCTTGAAGGTTTGTGATTTTCTTGACCTTCTTCTTCTT	2396
CYP52A1A	2881	TTACTTCTATCC - - - - - CCTGTATCCCTTATTATCCCTCTCAGTCACATGATTGCTGTAATTGTCGTGCAGGA	2948
CYP52A2A	2886	ATGTTTCCTTCCATCCT - - - - - GTCGAGTCAAAAGGAGTTTGTGTTGTAACTCCGGACGATGTTTAAATAG	2953
CYP52A2B	2774	TTGTTTCCTTCCATCCT - - - - - GTTGAGTCAAAAGGAGTTTGTGTTGTAACTCCGGACGATGCTTAGATAG	2841
CYP52A3A	2874	TCGTTGACG - - - - - TGCTCGCTCATCAGCACTGTTTGAAGACGAAAGA-GAAAAATTTTGTGTA	2930
CYP52A3B	2658	TTTTTCTTCCCTTACCTTCGTTGCTCGCTCATCAGCACTGTTTGAACGAAAAAGAAAAATTTTGTGTA	2727
CYP52A5A	2782	GAGTTGTCATCTT-GGGGAGATTACACCTTTTG-CAGCTCTCCGTATACACTTGTACTCTTTGTAAACCTC	2849
CYP52A5B	2818	G - - - - - CATCTTAG-GGAGAGATAGCACCTTTTG-CAGCTCTCCGTATACAGTTTACTCTTTGTAAACCTA	2881
CYP52A8A	2128	ATTGTAATAAATAG-TGTACACTAATTGTGGTGGCCGGAGATAAATTACAGTTTGGTTTGTGTAAACTC	2196
CYP52A8B	2588	AGTTCAGTAAT - - - - - TACACACTAATTGTGGTGGCCGGGATAAATTACCGTTTGGTTTGTGTAAAAAT	2654
CYP52D4A	2397	GAGCTTCTTTCCG - - - - - TCAAACTTGACAGAAATGGCCATCATTTACAGGAACAACCA-CGTACGACGGCCGG	2463

FIG. 15I-2

CYP52A1A	2949	CACAACTCCCTAACGGACTTAACCATAAACAAGCTCAGAACCATAGCCGACATCACTCCTTCTTCTC	3018
CYP52A2A	2954	AAGTCGATCTCCATGTGATTGTTTGTACTGTGATTATGTAATCTGCG-----GACGTTATA	3016
CYP52A2B	2842	AAGTCGATCTCCATGTGATTGTTT-GACTGCTACTCTGATTATGTAATCTGTAAGCCTAGACGTTATG	2910
CYP52A3A	2931	AACAACACTGTCCAAATTTACCCAACGTGAACCATATG--CAAATGAGCGGC-----CTTTCAA	2989
CYP52A3B	2728	AACAACATTGCCCAAACCTTACCCAACGTGAACCATTAACCAAATGAGCGGC-----CTTTCAA	2788
CYP52A5A	2850	TATCAATCATGTGGGGGGGGGTTCAATTGTTTGGC-CATGGTGGTGCAATGTTAAATCCGCC-AACTACC	2917
CYP52A5B	2882	TGCCAATCATGTGG-----GGATTCAATTGTTGCC-CATGGTGGTGCAATGCAAAATCCCCCAACTACC	2944
CYP52A8A	2197	GCGGATATCTCTGGC-----AGTTTCTCTTCTCCGC-AGCAGCTTTGCCACGGGTTTGCTCTGGGGCCAA	2260
CYP52A8B	2655	TCGGACATCTCTGGT-----GGTTTCCCTTCTCCGC-AGCAGCTTTGCCACGGGTTTGCTCTGGGGCCAA	2718
CYP52D4A	2464	TACCGCATCTGGAGTA---TCTCGCCGTCGTTCAAGTAG--CACGAAACAGCAACGACGTCAACCATCTG	2528

FIG. 15I-3

CYP52A1A	3019	TCTTCTCCAA	3088	TCTTCTCCAA
-CYP52A2A	3017	CAAGCATGTG	3079	CAAGCATGTG
CYP52A2B	2911	CAAGCATGTG	2975	CAAGCATGTG
CYP52A3A	2990	CTGGTCGCTG	3054	CTGGTCGCTG
CYP52A3B	2789	CTGGTCACTG	2853	CTGGTCACTG
CYP52A5A	2918	CAATCTCACAT	2986	CAATCTCACAT
CYP52A5B	2945	CAATCTCACAT	3005	CAATCTCACAT
CYP52A8A	2261	CAAAATTCAAA	2318	CAAAATTCAAA
CYP52A8B	2719	CAAAATTCGAA	2785	CAAAATTCGAA
CYP52D4A	2529	CTTCCCAATCT	2590	CTTCCCAATCT
CYP52A1A	3089	CCACCTGGAAG	3158	CCACCTGGAAG
CYP52A2A	3080	TCTTTGTTA	3144	TCTTTGTTA
CYP52A2B	2976	TCCATATTAT	3043	TCCATATTAT
CYP52A3A	3055	ACACCATAGA	3119	ACACCATAGA
CYP52A3B	2854	ACACCATAGA	2918	ACACCATAGA
CYP52A5A	2987	TTAGTAATT	3054	TTAGTAATT
CYP52A5B	3006	TTGGGGAAA	3073	TTGGGGAAA
CYP52A8A	2319	CTTGTGGGG	2386	CTTGTGGGG
CYP52A8B	2786	CTTGTGGGGG	2854	CTTGTGGGGG
CYP52D4A	2591	CCGCGTATAT	2658	CCGCGTATAT

FIG. 15J-I

CYP52A1A	3159	GTCCAAAGACGGCGAGTTCTGGTGTGCCCCGGAATCAGCCATCCCGGCCACATACAAGCAGCCGTTGATT	3228
CYP52A2A	3145	CAAAAAATGGGAAACTC--CAACAGACAAAA-AAAAAACTCCGAGCACTCCGAAACCCACAGAAACAATG	3211
CYP52A2B	3044	CAAAAGATGAGAAACTC--CAACAGAAAAAATAAAAAAATCCGAGCACTCCGAAACCAACAAAAACAATG	3111
CYP52A3A	3120	GAAGAATCAGCCAGA---AACTAGCGATGGATCCAAAGCCTGTGACCTTGCCCAATGGAGACGAAGTG	3185
CYP52A3B	2919	GAAGAATCGCGCCAGA---AACTAGCGATGGATCCAAAGCCTGTGGCCTTGCCCAATGGAGACGAAGTG	2984
CYP52A5A	3055	AGACAACCCAGAAAAAAGAAACAAATCCAGATAGAAAAACAAAGGGCT-GGACAACCATATAAT-AAAC	3122
CYP52A5B	3074	AGACAACCCAGAAAAA-----CAAAATCCAGATAGAAAGAAAGGGCT-GGACAACCATATAAT-AAAC	3135
CYP52A8A	2387	TTATGTCTGAGGCGTG---CTTGAAAGAAGTGTCAAAATGTGACAGGCG-ACGCTATTCGACAT-GAAC	2450
CYP52A8B	2855	TTATGTCTAAGGCGTG---CTTGACACAAGTGTCAAAAGGTGACAGGCG-ACGTTATTCGACAT-GAAC	2918
CYP52D4A	2659	CCACCACTGCCCTCGG-----TTGAGTCAAGGCAGTATGATGCCCGGGATCCAGTACTCCAATGGGAACC	2722
CYP52A1A	3229	GCGTGCACTACTCGGCGAGCCCAAAATGGAGCCACGCAATCGGACCATGAAGCAAAAGTACATTCAACGAGA	3298
CYP52A2A	3212	GGG---CGCCAGAAATTATTGACTATTGTGACTTTTAA-----CGCTAACGCTCATTCAGTG	3266
CYP52A2B	3112	GGG--GCGCCAGAAATTATTGACTATTGTGACTTTTAA-----ATTTTTCCGTTAACTTTCATTCAGTG	3177
CYP52A3A	3186	GAGTTGAACCAAGCGTTCCTAGAAGTTACCACATTAATGTCGAAATGAGTTTGACTTGGACCAATTGAACG	3255
CYP52A3B	2985	GAGTTGAACCAAGCGTTCCTAGAAGTTACCACATTAATGTCGAAACGAGTTTGACTTGGACCAATTGAACG	3054
CYP52A5A	3123	AATCTAGGGTCTACTCCATCTTCCACTGTTTCTTCTTCCAGACTTAGCT-AACAACAACACTCACTTCA	3191
CYP52A5B	3136	AACCTAGGGTCCACTCCATCTTCACT--TCTTCTTCTTCCAGACTTATCT-AACAACGACTCACTTCA	3201
CYP52A8A	2451	GCGAAAGGGTTATTTGCATCAATACGAG--GGGCTGACTCTAGTCTAGG--ATGGCAGTCTCCTAGGTTGC	2515
CYP52A8B	2919	GCAAAAGGGTAATTTGCATCGATACGAG--GGGTGCTCTGGTCTAAG--AAGGACCCCCCAGGTTGC	2983
CYP52D4A	2723	TCT----GCACGGTGTGCTGCAGTTTGTAGGGCGTATTTCGA-----TCCATGATCGTTCCTTTGG	2779

FIG. 15J-2

CYP52A1A	3299	TCACGGGTGTTTCAG-TGTGCGAGATTGAGAAAGTTCGACGATGGATGGAAGTACGATCTCGTTGCGGATT	3367
CYP52A2A	3267	TAGTGGGTCTTACACGG-----GGTATTGCTTTCTACAATGCAAGGCA-CAGTTGAAGGTTTGCACC	3328
CYP52A2B	3178	AAGTGTGTTACACGGGGTGGTGATGGTGTGGTTTCTACAATGCAAGGCA-CAGTTGAAGGTTTCCACA	3246
CYP52A3A	3256	CGGCAGAGTTGTTTACTA-CGCTGGCGACATATCTACAAGAAGGGCACATCAATCGCAGACAGTGCCA	3324
CYP52A3B	3055	CGCCGAGTTGTTTACTA-CGCCGGCGACATATCTACAAGAAGGGCACATCAATGCGACAGTGCCA	3123
CYP52A5A	3192	CCATGGATTACGCAGGCATCACGGGTGGTCCATCAGAGG-CGAGGCCCTTGAAGAACTCG--CAGAATT	3258
CYP52A5B	3202	CCATGGATTACGCAGGCATCACGGGTGGTCCATCAGAGG-CGAGGCCCTTGAAGAACTCG--CCGAGTT	3268
CYP52A8A	2516	AAACATGTTGCACCA-TATCCCTCCTGGAGTTGGTCGAC--CTCGCCTACGCC-ACCCTCA--GCGATCG	2579
CYP52A8B	2984	AAACATGTTGCACCTG-CATCCCACTCAGAGTTGGTCGAC--CACGCCCTACGCTTACCCTCA--GCGATCG	3048
CYP52D4A	2780	TGCTGTAGTATAACGAGCT--CTTGGTGTCTCTTGAAATGGAACAGGTTGGATGTGTGTTGAGTTTGTCCT	2847

FIG. 15J-3

CYP52A1A	3368	ACGACTTCGGTGGGTTGTTATCTAAACGAAGATTTCTATGAGACGCAGCATGTGTTTCGGTTCGAGGATTG	3437
CYP52A2A	3329	TAACGTTGCCCCGTGTCAACTCAATTTGAC-----G--AGTAACTTCTTAAGCTCGAATTATGC	3385
CYP52A2B	3247	TAACGTTGCACCATATCAACTCAATTTATC-----CTCATTCATGTGATAAAAGAAGACCCAAA	3305
CYP52A3A	3325	GATTGTCTTATTATTGAGAGCAAACTAC-----ATCTTGAACATACCTTGGGTATTTTGAT	3379
CYP52A3B	3124	GATTGTCTTACTATTGAGAGCAAACTAC-----ATCTTGAACATACCTTGGGTACTTTTAT	3178
CYP52A5A	3259	G-ACCATCCAGAACCCAGCCATCCAGCT-----TGAAAGAAATCAACACCCGGCATCCAGAAGGACGACTT	3321
CYP52A5B	3269	G-ACCATCCAGAACCCAGCCATCCAGCT-----TGAAAGAAATCAACACCCGGCATCCAGAAGGACGACTT	3331
CYP52A8A	2580	GCACTTTCCGTTGTTCAATATTCTC-----CTTCCCATTTGTTCCAGGGTTA--TC	2629
CYP52A8B	3049	GCACTTTCCGTTGTTCAATATTCTCT-----CCCCCCTGCTTCCCCCATTTGTTCCAGGGATTA--TC	3110
CYP52D4A	2848	CGGTGCTTGTTTGCAAGTCTTCGATCG-----ACCGTAGTGAGTAGACAGTTGGCGGG	2901
CYP52A1A	3438	TGCGTACGTCATGAGTGTGCCTTTTGTATGGACCCCAAGGAGGAAGGTTACGTGTTGGGACGTACAGATCC	3507
CYP52A2A	3386	AGCT-CGTGCGTCAACCTATGTGCAGGAAGAAAAATCCAAAA--AATCGAAA-ATGCGACTTTCGAT	3451
CYP52A2B	3306	AGGT-AAT-TGGCAGACCCCCCAAGGGAAACACGGAGTAGAAAGC--AATGGAAACACGCCCATGACAGT	3371
CYP52A3A	3380	TTTCG-AAGCAGGGATTGGATTTGATAGTCACGGACAACACGCGCT--TGTTTTGATAGTATTTTGAAAAAGT	3446
CYP52A3B	3179	TTTCG-AAGCAGCGATTGGATGTGATAGTCACCGACAACAACGCGT--TGTTTTGATAATATTTTGAAAAAGT	3245
CYP52A5A	3322	TGCC-AAGTTGTTGTCTGCCACCCCGAAAAATCCCCACCAAGCACA--AGTTGAACGGCAACCCAGAAATT-	3387
CYP52A5B	3332	TGCC-AAGTTGTTGTCTTCCACCCCGAAAAATCCAACCAAGCACA--AGTTGAATGGCAACCCAGAAATT-	3397
CYP52A8A	2630	AACA-ACGTTGCCGGCCTCCTC-----CCCAAATTA-----CAAGAAAAATAAAATT-	2674
CYP52A8B	3111	AACA-ACGTTGCCGGTCTCCTCTCCCCCCCCCTCCCCCAGTTAT-----GTACAAGAAAAATAAATT-	3171
CYP52D4A	2902	GGTGGTGGCTCGGGCTTTATTCTGTGTTTGTGTTTCTTCTTAGT--CTTGGAAATGACGCTGTTATCGAC	2969

**FIG. 15K-1**



CYP52A1A	3508	ATTGAAAGGTTGAGCTGGGGTAAAGACGGGGACGTGGA-GTGGACCATGG---CGACGACGTGCGATCCT	3573
CYP52A2A	3452	TTTGAATAAACCAAAAGAAAAATGTCGCACTTTTTC-----TCGCTCTCGCTCTCTCGACCCAAATCA	3516
CYP52A2B	3372	GCCATTTAGCCCA--ACACATCTAGTATTCTTTT-----TTTTTTTGTGGCAGGTGCACACCTGG	3433
CYP52A3A	3447	TTTGAAAAGATCTAC---AAGTTGATAAGCGTGTGA-----ACGATATGATTGACAAACGCAAAAGGTGA	3507
CYP52A3B	3246	TTTGAAAAGATCTAC---AAGTTGATAAGCGGTGA-----ACGATATGATTGACAAACGCAAAAGGTGA	3306
CYP52A5A	3388	GTCTGAGGTCGCCATTGCCAAAAGAGGTACGAGGTGTGATTGCCTTGAGCGACGCCACAAAAGACCCA	3457
CYP52A5B	3398	GTCCGAAGTCGCCATTGCCAAAAGAGGTACGAGGTGTGATTGCCTTGAGCGACGCCACGAAAGAACCA	3467
CYP52A8A	2675	GTGCGACGGCACCGATCTGTCAAAGATACAGATAA-----ACCTTAAATCTGCAAAAACAAGACCCC	2736
CYP52A8B	3172	GTGCGACGGCACCGATCTGTCAAAGATACAGATAA-----ACCTTAA-----TCC	3216
CYP52D4A	2970	GGTTCGTAGTATAAGTAGCGCCAATATGAGAATGTATA-----TCCGCATCACCAAGACTCTTCAGCCT	3034
CYP52A1A	3574	GGTGGGTTTATCCCGCA-ATGGATAACTCGATTGAGCA-TCCCTGGAGCAATCGCAAAAGATGTGCCTAG	3641
CYP52A2A	3517	CAACAAATCCTCGCGCGCAGTATTTCGACGAAAC--CACAAACAATAAAAAAACAATTTCTACACCACT	3584
CYP52A2B	3434	ACTTTAGTTATTGCCC-CATAAAGTTAAACAATCT--CACCTTTGGCTCTCCAGTGTCTCCGCCCTCCAGA	3500
CYP52A3A	3508	CAAGCGACATCAACAGTCTAGCATTCATCAATTG--CATCAACTACTCGAGAGGTCAACTATTCTCCGCA	3575
CYP52A3B	3307	CAAGCGACATCAACAGTCTAGCATTTATCAACTG--CATCAACTACTCGAGGGGTCAACTATTCTCCGCA	3374
CYP52A5A	3458	ATCAAAGTGACCTCCAGATCAAGATCTTGATTGACAAGTTCAAGGTGTACTTGT---TTGAGTTGCCTG	3524
CYP52A5B	3468	ATCAAAGTGACCTCCAGATCAAGATCTTGATTGACAAGTTCAAGGTGTACTTGT---TTGAGTTGCCCG	3534
CYP52A8A	2737	TCCCCATAGCCTAGAAGCACCAAGATGATGGAGCAACTCTCCAGTACTGGTACATCGCACTCTCTG	2806
CYP52A8B	3217	CTCCCATAGCCTAGAAGCATCAAAAAGATGATTGAGCAACTCTCCAGTACTGGTACATTCGACTCCCTG	3286
CYP52D4A	3035	GTTACAACGACTGAGGCTGTTGGCCGTGTGACCAATTGGTTTCTTTGGTGACCTAGATTGGTCCCGCAGG	3104

FIG. 15K-2

CYP52A1A	3642	TG---	TATTAAACTACATACAGAAATAAAACG	TGCTTGATTCATTGGTTT	--GGTTCTTGTGGGTT	3705
CYP52A2A	3585	T----	CTTTTCTTCA	CCAGTCAACAAAAACAACAAAT	TATACACCATTTCAACGATTTT	3650
CYP52A2B	3501	TG---	CTCGTTT	TACACCCCTCGAGCTAACGACAAACA	CAACCCATGAGGGAATGGGCAAGTT	3562
CYP52A3A	3576	CA---	CGAACTTTTGGG	-ACTGGTTT	TGTTGGATTGGTCGACATCTATTTCAACCAAGTT	3641
CYP52A3B	3375	CA---	CGAACTTTTGGG	-ACTGGTTT	TGTTGGATTGGTCGACATCTATTTCAACCAAGTT	3440
CYP52A5A	3525	AC---	CAGAAAGTTCTCCTACTCCATCGTGTC	CAACTCGCCCCC	-TGGACCTTGCCTCGGG	3590
CYP52A5B	3535	AC---	CAGAAAGTTCTCCTACTCCATCGTGTC	CAACTCGCCCCC	-TGGACCTTGCCTCGGTG	3600
CYP52A8A	2807	TA---	TGGTTCACTTCGCTACTTGGCTTCC	CACGACGAGCCGCTACTTG	-CGCCACAAGCTCGGCG	2872
CYP52A8B	3287	TA---	TGGTTCACTTCGCTACTTGGCTTCC	CACGACGAGCCGCTACTTG	-CGCCACAAGCTCGGCG	3352
CYP52D4A	3105	GAAAGCAAGGCTGCTAGGGGGGCATAC	CAAAACAAGGTCGTGTAAATCAGTATCT	ATGATGCTACCATGTG		3174

FIG. 15K-3

FIG. 15L-1

CYP52A1A	3844	GTGTGTTTGCTCTTGTGATGACAAATGATGTATTTGTACGATACCTGAAATAATAAAACATCCAGT	3913
CYP52A2A	3788	GTCGAAATAGACGGTTTGTCTTACTCATTAGATGGTCCAGATTACTTTTCAAGCCAAAGTCTCT-CGAGTT	3856
CYP52A2B	3693	TTGCTTTTGTCTTTTGTCTTTTGCACT---CTCTCCCACTCCCACAATCAGTGCAGCAACACA-CAA	3755
CYP52A3A	3779	GTTCTACAAGTACATCACTTCAACAGT--GTCACGAGACTACAACTCCAACATCGGCTCCACAGCCAAAAG	3846
CYP52A3B	3578	GTTCTACAAGTACATCACTTCAACAGT--GTCGCAAGACTACAACCTCCAACATCGGAGCCACAGCCAAAAG	3645
CYP52A5A	3723	TGACCTTGTGCGGTGTGTGGACGGGTGATTGACCATGCC-AACTTCTTGAGCGTGTCTCGCGGACCT	3791
CYP52A5B	3733	TGACCTTGTGCGGTGTGTGGACGGGTGATTGACCATGCC-AACTTCTTGAGCGTGTCTCGCGGACCT	3801
CYP52A8A	3002	CCTTCTCGAGCTACACTTTTCGGCATCCATATCATCTTACC-CGGGACCCGGAGAACATCAAGCGGTCT	3070
CYP52A8B	3485	CTTCTCGAGCTATACCTTTCGGCATCCATATCATCTTACT-CGGGACCCGGAGAACATCAAGCGGTCT	3553
CYP52D4A	3313	CCCAATCAGCCATTCCCCTGCGGAATATAAATTCAAC	3348
CYP52A1A	3914	CATTGAGCTTATTACTCGTGAACCTTATGAAAGAACTCATTCAGCCGTTCCCAAAAAACCCAGAAATTGAA	3983
CYP52A2A	3857	TTGTTTGCTGTTTCCCCCAATTCCCTAACTATGAAGGGTTTTTATAAGGTCCAAAGACCCCAAGGCATAGTT	3926
CYP52A2B	3756	ATGATATCGATTTGTCCAAAACCCAAACTCAGTGGCTTTGAGGTGTGACGAGTT	3755
CYP52A3A	3847	ATGATATCGATTTGTCCAAAAGCC	3900
CYP52A3B	3646	TCAAAGATCTTCTTGAACCTTGGA CTGGTATGTGGAC	3663
CYP52A5A	3792	TCAAAGATCTTCTTGAACCTTGGA CTGGTATGTGGAC	3826
CYP52A5B	3802	TGCGGACGCAGTTCGATGACTTCTCGCTCGGTGGCAGGATCAGGTTCTTGAAGCCGTTGTTGGGGTATGG	3871
CYP52A8A	3071	TGCGGACGCAGTTCGATGACTTCTCGCTCGGTGGCAGGATCAGGTTCTTGAAGCCGTTGTTGGGGTATGG	3140
DYP52A8B	3554	TGCGGACGCAGTTCGATGACTTTTTCG	3579
CYP52D4A	3349		3348

FIG. 15L-2

CYP52A1A	3984	GATCTTGCTCAACTGGTCA	4053
CYP52A2A	3927	TGCAAGTAGTAGATCGCCATGATCTGATAC	3948
CYP52A2B	3756	TTTCTTCTTCTTCTTCTG	3755
CYP52A3A	3901		3900
CYP52A3B	3669		3668
CYP52A5A	3827		3826
CYP52A5B	3872	CGACTTTTGTACGACGAGCCGACGAGTACCAGAACTT	3910
CYP52A8A	3141	GATATTCACGTT	3152
CYP52A8B	3580		3579
CYP52D4A	3349		3348

FIG. 15L-3

CYP52A1A	4054	AGTTCTCCACGTACGGCAAGTACGGCAACGAGCTCTGGAAGCTTTGTTGTTGGGGTCATA	4115
CYP52A2A	3949		3948
CYP52A2B	3756		3755
CYP52A3A	3901		3900
CYP52A3B	3669		3668
CYP52A5A	3827		3826
CYP52A5B	3911		3910
CYP52A8A	3153		3152
CYP52A8B	3580		3579
CYP52D4A	3349		3348

FIG. 15M

CYP52A1A	1	MATQEIIDSVLPLYL-----TKWYTVITAAVLVFLISTNIKNYV	38
CYP52A2A	1	MTVHDI IATY-----FTKWYVIVPLALIAAYRVLDFYGRY	35
CYP52A2B	1	MTAQDI IATY-----ITKWYVIVPLALIAAYRVLDFYGRY	35
CYP52A3A	1	MSSSPSFAQAEVLATTSPIEYFLDNTRYRWYFIPLVLLSLNFISLLHTRY	50
CYP52A3B	1	MSSSPSFAQAEVLATTSPIEYFLDNTRYRWYFIPLVLLSLNFISLLHTRY	50
CYP52A5A	1	MIEQLLEY-----WYVVVPVLYIIKQLLAYTKTRV	30
CYP52A5B	1	MIEQILEY-----WYIVVPVLYIIKQLLAYSKTRV	30
CYP52A8A	1	MLDQILHY-----WYIVPLPLAIINQIVAHVRTNY	30
CYP52A8B	1	MLDQIFHY-----WYIVPLPLVIIKQIVAHARTNY	30
CYP52D4A	1	MAISSLLSWD-----VICVVFICVCYFGYEYCYTKY	32
CYP52A1A	39	KAKKCLKVDPPPYLKDAGLTGILSLIAAIKAKNDGRLANFAD---EVFDEY	85
CYP52A2A	36	LMYKLGAKPFFQKQTDGCFGFKAPLELLKKSDGTLDFTL---QRIHDL	82
CYP52A2B	36	LMYKLGAKPFFQKQTDGYFGFKAPLELLKKKSDGTLDFTL---ERIQAL	82
CYP52A3A	51	LERRFHAKPLGNFVRDPTFGIATPLLLIYLKSKGTMKFAWGLWNNKYIV	100
CYP52A3B	51	LERRFHAKPLGNVVLDPTFGIATPLLIIYLKSKGTMKFAWSFWNNKYIV	100
CYP52A5A	31	LMKKLGAAPVTNKLVDNAFGIVNGWKALQFKKEGRAQEYND---YKFDHS	77
CYP52A5B	31	LMKQLGAAPITNQLYDNVFGIVNGWKALQFKKEGRAQEYND---HKFDSS	77
CYP52A8A	31	LMKKLGAKPFTHVQRDGLWLFKFGREFLKAKSAGRLVDLII---SRFHDN	77
CYP52A8B	31	LMKKLGAKPFTHVQLDGLWFGFKFGREFLKAKSAGRQVDLII---SRFHDN	77
CYP52D4A	33	LMHKHGAREIENVINDGFFGFRLLPLLMRASNEGRLLIEFSV---KRFESA	79

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CYP52A1A	86	PN--HTFYLSVAGALKIVMTVDPENIKAVLATQFTDFSLGTRHAFAPLL	133
CYP52A2A	83	DRPDIPTFTFPVFSINLVNTLEPENIKAILATQFNDFSLGTRHSHFAPLL	132
CYP52A2B	83	NRPDIPTFTFPVFSINLVNTLEPENIKAILATQFNDFSLGTRHSHFAPLL	132
CYP52A3A	101	RDPKYTTGLRIVGLPLIETMDPENIKAVLATQFNDFSLGTRHDFLYSLL	150
CYP52A3B	101	KDPKYTTGLRIVGLPLIETMDPENIKAVLATQFNDFSLGTRHDFLYSLL	150
CYP52A5A	78	KNPSVGTYSILFGTRIVVTKDPENIKAILATQFGDFSLGKRHTLTKPPLL	127
CYP52A5B	78	KNPSVGTYSILFGTKIVVTKDPENIKAILATQFGDFSLGKRHALFKPPLL	127
CYP52A8A	78	ED----TFSSYAFGNHVFTTRDPENIKALLATQFGDFSLGSRVKKFKPPLL	123
CYP52A8B	78	ED----TFSSYAFGNHVFTTRDPENIKALLATQFGDFSLGSRVKKFKPPLL	123
CYP52D4A	80	PHPQNTLVNRALSVPVILTKDPVNIKAMLSQFDDFSLGLRLHQFAPLL	129
		.. * * * * * * * * * * * * * *	
CYP52A1A	134	GDGIFTLDGEGWKHSRMLRPQFARDQIGHVKALEPHIQIMAKQIKLNQ	183
CYP52A2A	133	GDGIFTLDGAGWKHSRMLRPQFAREQISHVKLLEPHVQVFFKHVRKAQ	182
CYP52A2B	133	GDGIFTLDGAGWKHSRMLRPQFAREQISHVKLLEPHVQVFFKHVRKAQ	182
CYP52A3A	151	GDGIFTLDGAGWKHSRMLRPQFAREQISHVKLLEPHVQVFFKHVRKH	200
CYP52A3B	151	GDGIFTLDGAGWKHSRMLRPQFAREQISHVKLLEPHVQVFFKHVRKH	200
CYP52A5A	128	GDGIFTLDGEGWKHSRMLRPQFAREQVAHVTSLEPHFQLLKKHILKH	177
CYP52A5B	128	GDGIFTLDGEGWKHSRMLRPQFAREQVAHVTSLEPHFQLLKKHILKH	177
CYP52A8A	124	GYGIFTLDAEGWKHSRMLRPQFAREQVAHVTSLEPHFQLLKKHILKH	173
CYP52A8B	124	GYGIFTLDGEGWKHSRMLRPQFAREQVAHVTSLEPHFQLLKKHILKH	173
CYP52D4A	130	GKGIFTLDGPEWKQRSMLRPQFAKDRVSHILDLEPHFVLLRKHIDHNG	179
		* * * * * * * * * * * * * *	

FIG. 16A-2

CYP52A1A	184	KTFDIQELFFRFTVDTATEFLFGESVHSLYDEKLGITP-NEIPGRENFA	232
CYP52A2A	183	KTFDIQELFFRLTVDSATEFLFGESVESLRDESIGMSINALDFDGKAGFA	232
CYP52A2B	183	KTFDIQELFFRLTVDSATEFLFGESVESLRDESIGMSINALDFDGKAGFA	232
CYP52A3A	201	QTFDIQELFFRLTVDSATEFLFGESAESLRDESIGLPTTKDFDGRRDFA	250
CYP52A3B	201	QTFDIQELFFRLTVDSATEFLFGESAESLRDDSVGLTPTTKDFEGRGDFA	250
CYP52A5A	178	EYFDIQELFFRFTVDSATEFLFGESVHSLKDESIGINQDDIDFAGRKDFA	227
CYP52A5B	178	EYFDIQELFFRFTVDSATEFLFGESVHSLKDETINGINQDDIDFAGRKDFA	227
CYP52A8A	174	EYFDIQELFFRFTVDSATEFLFGESVHSLKDEEIGYDTKDMSEERRR-FA	222
CYP52A8B	174	EYFDIQELFFRFTVDSATEFLFGESVHSLRDEEIGYDTKDMAEERRK-FA	222
CYP52D4A	180	DYFDIQELYFRFMDVATGFLFGESVGLKDE-----D-----ARFL	216
		***** ** * ** ***** ** * *	
			*
CYP52A1A	233	AAFNVSQHYLATRSYSQTFYFLTNPKEFRDCNAKVHHLAKYFVNKALNFT	282
CYP52A2A	233	DAFNYSQNYLASRAVMQQLYWVLNGKKFKECNAAKVHKFADYYVVKALDLT	282
CYP52A2B	233	DAFNYSQNYLASRAVMQQLYWVLNGKKFKECNAAKVHKFADYYVVKALDLT	282
CYP52A3A	251	DAFNYSQTYQAYRFLQMQMYWILNGSEFRKSIIVHKFADHYVQKALELT	300
CYP52A3B	251	DAFNYSQTYQAYRFLQMQMYWILNGAEFRKSIIVHKFADHYVQKALELT	300
CYP52A5A	228	ESFNKAQEYLAIRTLVQTFYWLNNKEFRDCTKLHKFTNYVYVQKALDAS	277
CYP52A5B	228	ESFNKAQEYLSIRILVQTFYWLNNKEFRDCTKLHKFTNYVYVQKALDAT	277
CYP52A8A	223	DAFNKSQVYVATRVVALQNLWLNNKEFECNDIVHKFTNYVYVQKALDAT	272
CYP52A8B	223	DAFNKSQVYLSSTRVALQTLWLNNKEFECNDIVHKFTNYVYVQKALDAT	272
CYP52D4A	217	EAFNESQKYLATRATLHELFLYFLCDGFRFRQYKVVVKFCSCQVHKALDVA	266
		*** ** * * * * * * * * * * * * * * *	

FIG. 16B-I



CYP52A1A	283	PEELEKSKSGYVFLYELVKQTRDPKVLQDQLLNIMVAGRDTTAGLLSFA	332
CYP52A2A	283	PEQLE-K-QDGYVFLYELVKQTRDKQVLRDQLLNIMVAGRDTTAGLLSFV	330
CYP52A2B	283	PEQLE-K-QDGYVFLYELVKQTRDRQVLRDQLLNIMVAGRDTTAGLLSFV	330
CYP52A3A	301	DDDLQ-K-QDGYVFLYELAKQTRDPKVLQDQLLNILVAGRDTTAGLLSFV	348
CYP52A3B	301	DDDLQ-K-QDGYVFLYELAKQTRDPKVLQDQLLNILVAGRDTTAGLLSFV	348
CYP52A5A	278	PEELE-K-QSGYVFLYELVKQTRDPNVLRDQSLNILLAGRDTTAGLLSFA	325
CYP52A5B	278	PEELE-K-QGGYVFLYELVKQTRDPKVLQDQSLNILLAGRDTTAGLLSFA	325
CYP52A8A	273	PEELE-K-QGGYVFLYELVKQTRDPKVLQDQSLNILLAGRDTTAGLLSFA	320
CYP52A8B	273	PEELE-K-QGGYVFLYELAKQTKDPNVLRDQSLNILLAGRDTTAGLLSFA	320
CYP52D4A	267	PEDTS----EYVFLRELVKHTRDPVVLQDQALNVLLAGRDTTASLLSFA	311
		**** ** * * * * * ****	
CYP52A1A	333	LFELARHPMWSKLREEIEVNFVGEDSRVEEITFEALKRCEYLKAILNE	382
CYP52A2A	331	FFELARNPEVTNKLREEIEDKFGLGENASVEDISFESLKSCEYLKAVLNE	380
CYP52A2B	331	FFELARNPEVTNKLREEIEDKFGLGENARVEDISFESLKSCEYLKAVLNE	380
CYP52A3A	349	FYELSRNPEVFAKLREEEVENRFGLGEEARVEEISFESLKSCEYLKAVINE	398
CYP52A3B	349	FYELSRNPEVFAKLREEEVENRFGLGEEARVEEISFESLKSCEYLKAVINE	398
CYP52A5A	326	VFELARHPEIWAKLREEIEQQFGLGEDSRVEEITFESLKRCEYLKAFLE	375
CYP52A5B	326	VFELARNPHIWAKLREEIEQQFGLGEDSRVEEITFESLKRCEYLKAFLE	375
CYP52A8A	321	VFELARNPHIWAKLREEIEQQFGLGEDSRVEEITFESLKRCEYLKAVLNE	370
CYP52A8B	321	VFELARNPHIWAKLREEIESHFGLGEDSRVEEITFESLKRCEYLKAVLNE	370
CYP52D4A	312	TFELARNDHMRKLREEVILTMGPSSD---EITVAGLKSCRYLKAILNE	357
		***. * **** * . * * * * *	

FIG. 16B-2

CYP52A1A	383	TLRMYPSPVNFRTATRDTTTLPRGGGANGTDPIYIPKGSTVAYVVYKTHR	432
CYP52A2A	381	TLRLYPSVPQNFRTATKNTTLPRGGKDGSLPVLVRKGQTVIYGVAHR	430
CYP52A2B	381	TLRLYPSVPQNFRTATKNTTLPRGGKDGSLPVLVRKGQTVMYGVYAAHR	430
CYP52A3A	399	TLRLYPSVPHNFRTATKNTTLPRGGGEDGYSPIVVKKGQVVMYTVIATHR	448
CYP52A3B	399	ALRLYPSVPHNFRTATKNTTLPRGGKDGCSPIVVKKGQVVMYTVIGTHR	448
CYP52A5A	376	TLRIYPSVPRNFRTATKNTTLPRGGSDGTSPILIQGEAVSYGINSTHL	425
CYP52A5B	376	TLRVYPSVPRNFRTATKNTTLPRGGGPDGTQPIILIQGEGVSYGINSTHL	425
CYP52A8A	371	TLRLHPSVPRNARFAIKDNTTLPRGGGPNKDPILIRKDEVVQYSISATQT	420
CYP52A8B	371	TLRLHPSVPRNARFAIKDNTTLPRGGGPNKDPILIRKNEVVQYSISATQT	420
CYP52D4A	358	TLRLYPSVPRNARFATRNNTTLPRGGGPDGSFPILIRKGQPVGYFICATHL	407
		.. ** * * * * * * * * * * * * * * * * *	
CYP52A1A	433	LEYYGKDANDFRPERWFEPSTKLGWAYVVPFNGGPRVCLGQQFALTEAS	482
CYP52A2A	431	NPAVYGKDALEFRPERWFEPETKLGWAFLPFNGGPRICLGQQFALTEAS	480
CYP52A2B	431	NPAVYGKDALEFRPERWFEPETKLGWAFLPFNGGPRICLGQQFALTEAS	480
CYP52A3A	449	DPSIYGADADVFRPERWFEPETKLGWAYVVPFNGGPRICLGQQFALTEAS	498
CYP52A3B	449	DPSIYGADADVFRPERWFEPETKLGWAYVVPFNGGPRICLGQQFALTEAS	498
CYP52A5A	426	DPVYGGPDAAEFRRPERWFEPSTKLGWAYLFPFNGGPRICLGQQFALTEAG	475
CYP52A5B	426	DPVYGGPDAAEFRRPERWFEPSTKLGWAYLFPFNGGPRICLGQQFALTEAG	475
CYP52A8A	421	NPAYYGADAADFRPERWFEPSTRNLGWAFLPFNGGPRICLGQQFALTEAG	470
CYP52A8B	421	NPAYYGADAADFRPERWFEPSTRNLGWAYLFPFNGGPRICLGQQFALTEAG	470
CYP52D4A	408	NEKVYGNDSHVFRPERWAALGKSLGWSYLPFNGGPRSCLGQQFAILEAS	457
		** * * * * * * * * * * * * * * * * *	

FIG. 16C-I

CYP52A1A	483	YVITRLAQMFETVSSDPGLEYPppKCIHLTMSHNDGVFVKM	523
CYP52A2A	481	YVTVRLQEFFAHLSMDPDTEYPPKMSHLTMSLFDGANIEM	522
CYP52A2B	481	YVTVRLQEFGLHLSMDPNTEYPPKMSHLTMSLFDGANIEM	522
CYP52A3A	499	YVTVRLQEFFAHLSMDPDTEYPPKLQNTLTLSLFDGADV	540
CYP52A3B	499	YVTVRLQEFGLHLSLDPNAEYPPKLQNTLTLSLFDGADV	540
CYP52A5A	476	YVLVRLVQEFSSHRLDPDEVYPPKRLTNLTMLCLQDGAIV	517
CYP52A5B	476	YVLVRLVQEFSSHRLDPDEVYPPKRLTNLTMLCLQDGAIV	517
CYP52A8A	471	YVLVRLVQEFPNLSQDPETKYPppRIAHLTMLCLFDGAHV	512
CYP52A8B	471	YVLVRLVQEFPSLSQDPETEPYPPRIAHLTMLCLFDGAYV	512
CYP52D4A	458	YVLARLTQCYTTIQLR-TTEYPPKKLVHLTMSLLNGVYIR	499

**FIG. 16C-2**

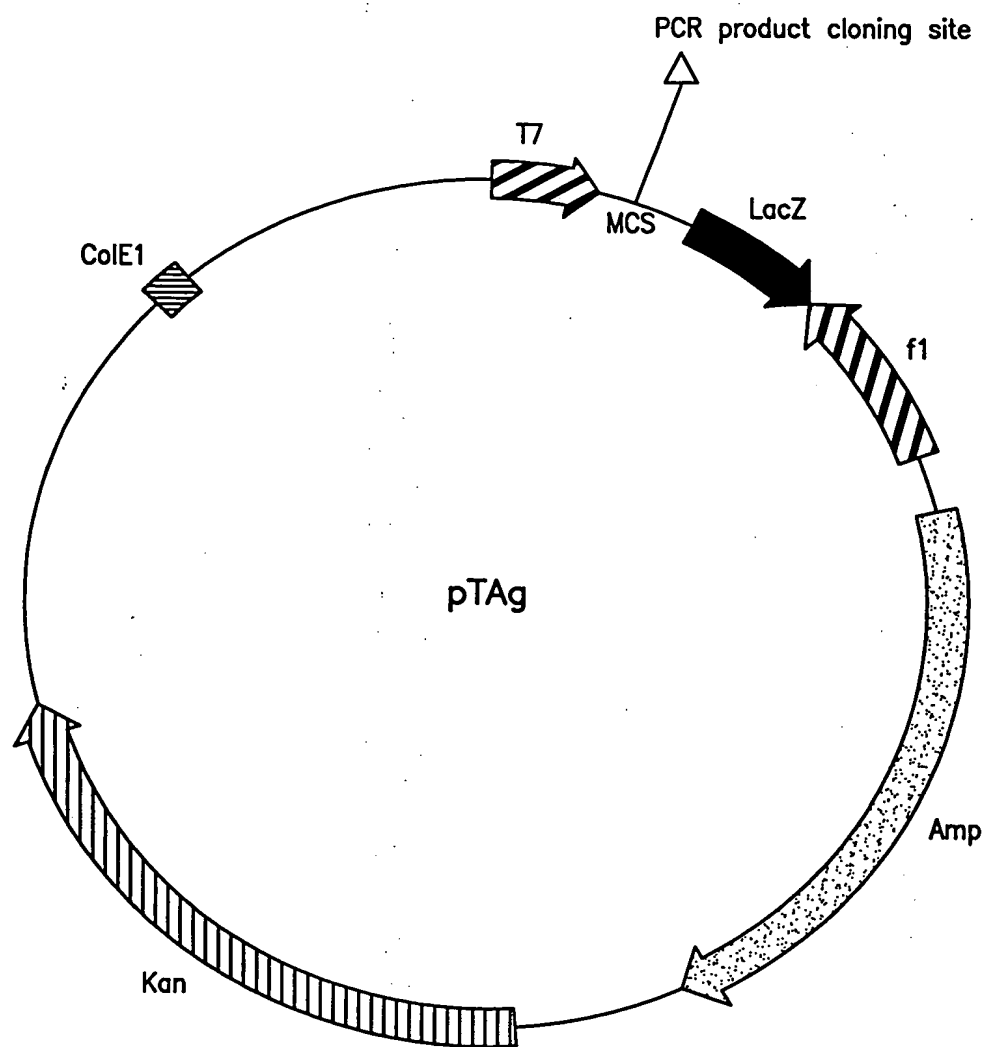


FIG. 17

100407 00002550

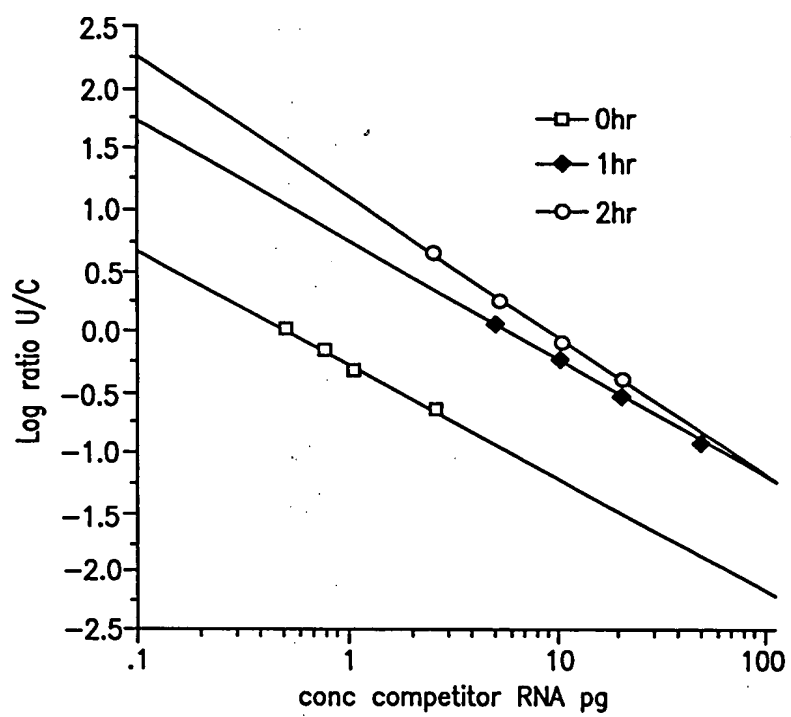


FIG. 18

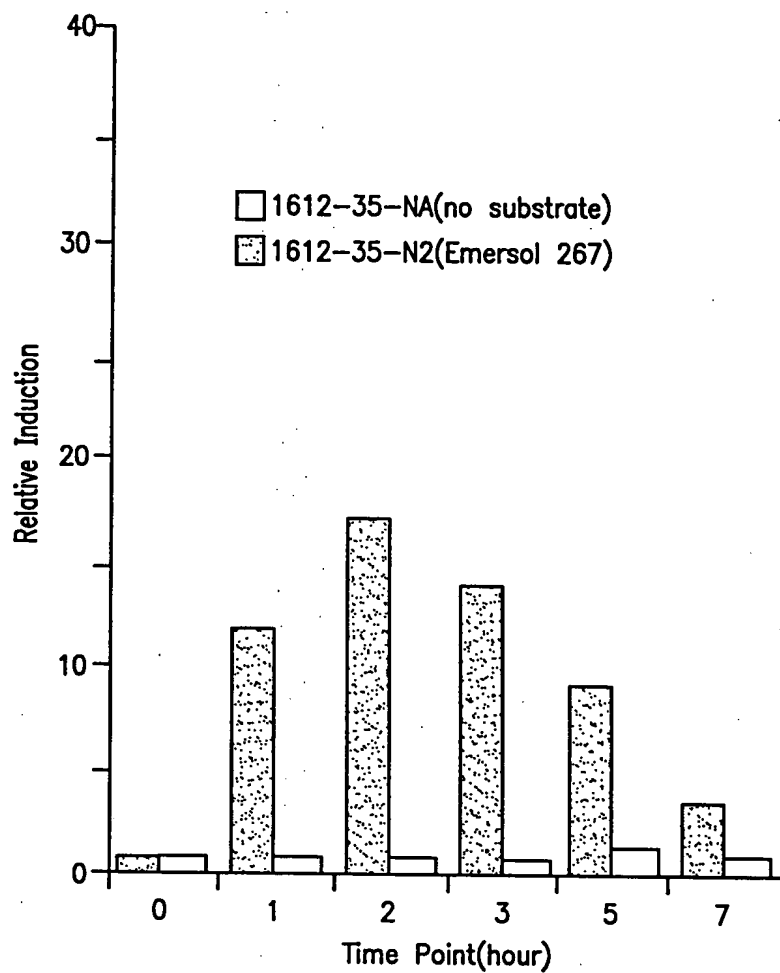


FIG. 19

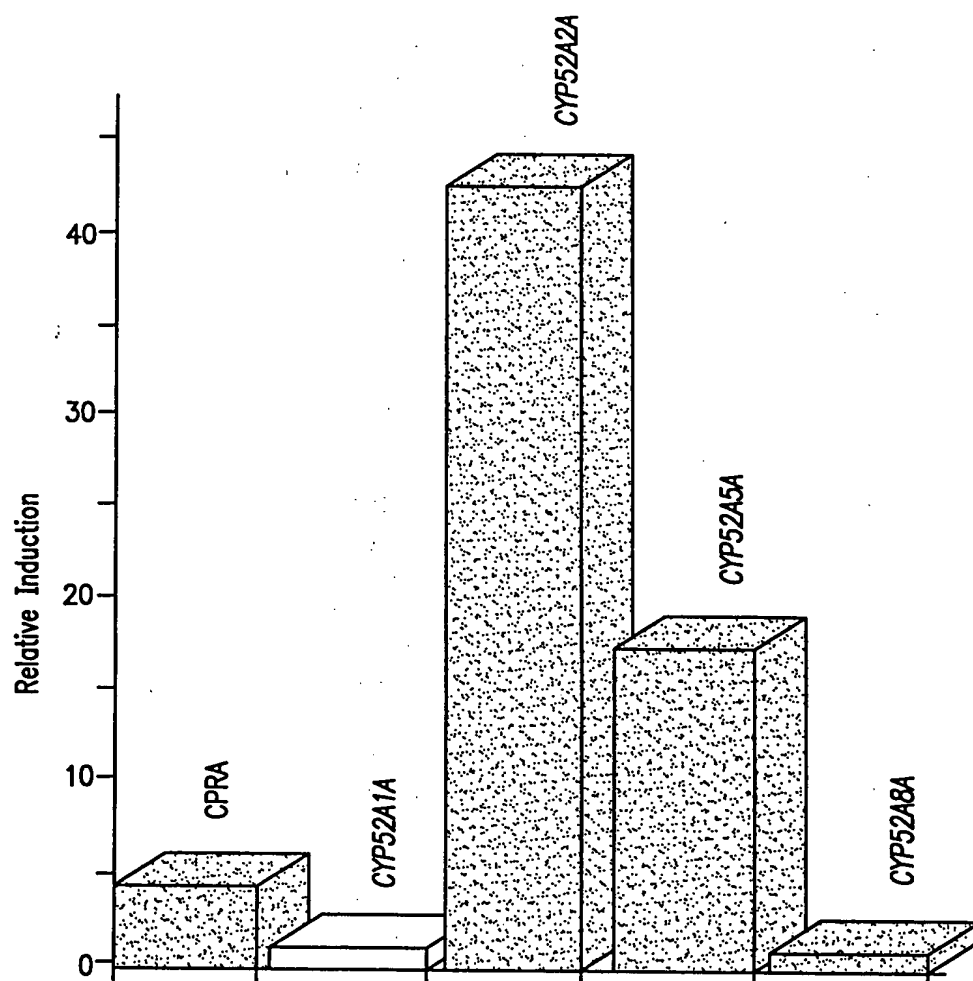


FIG. 20

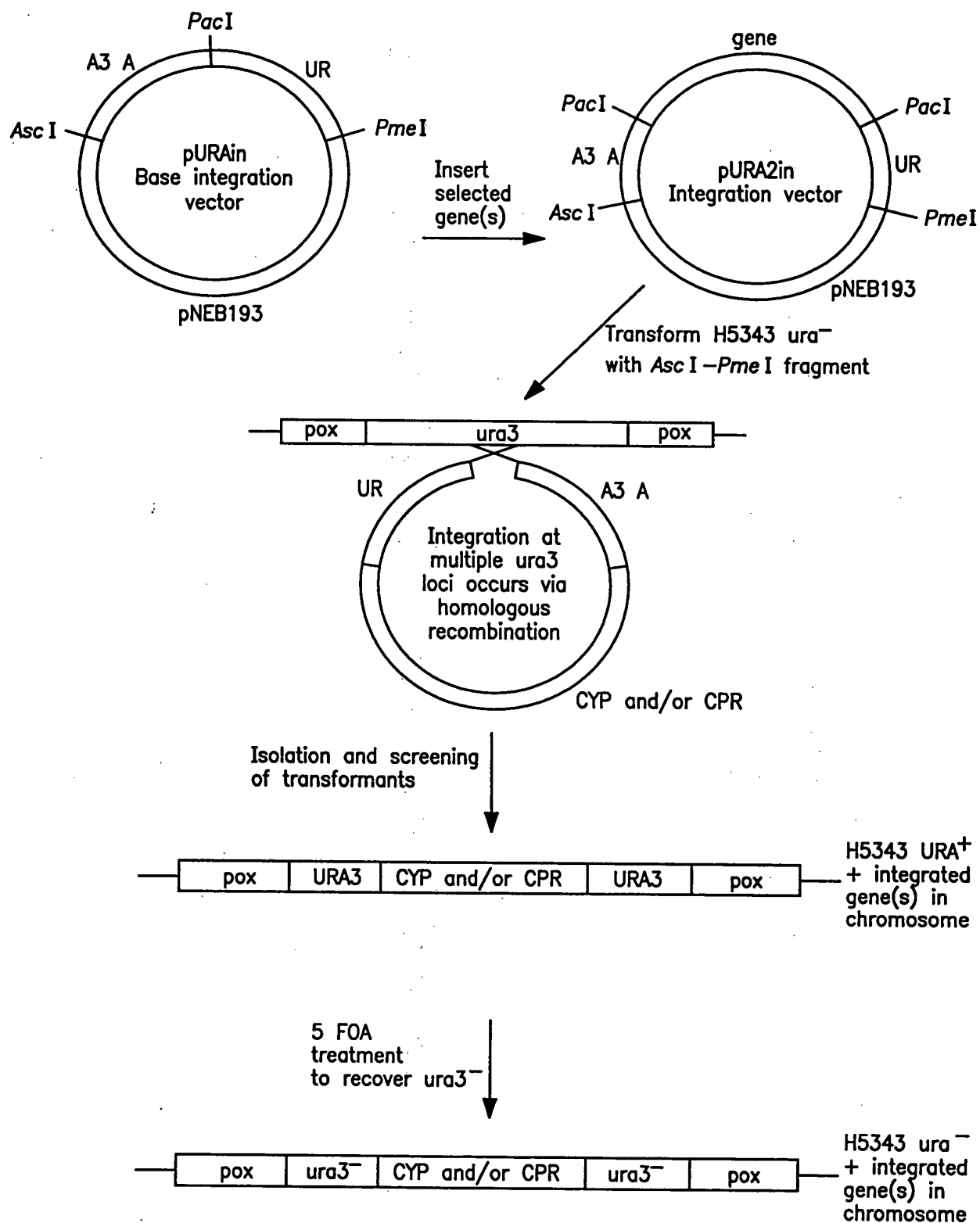


FIG. 21



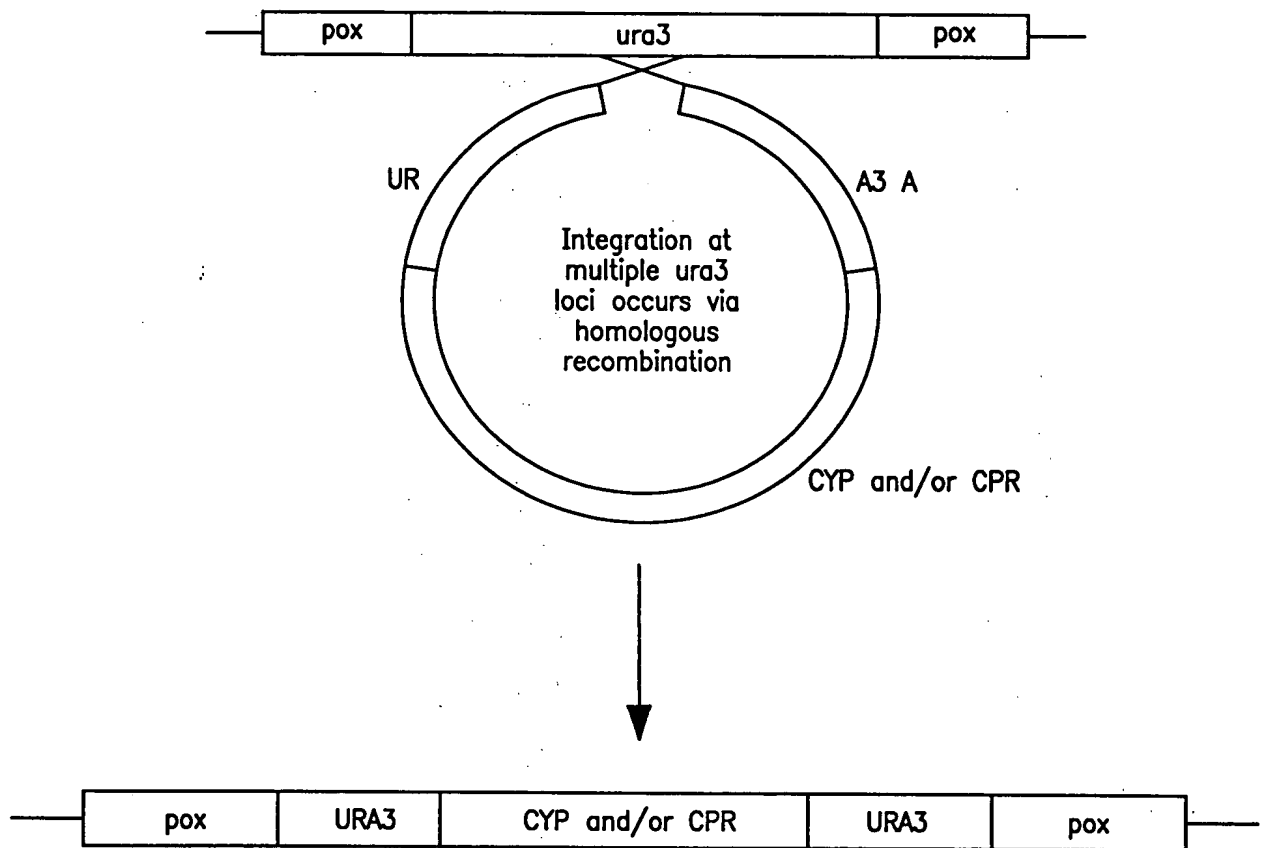


FIG. 22

Sequence Range: 1 to 1712

10	20	30	40	50	50	70	80
GGTACCGAGC	TCACGAGTTT	TGGGATTTC	GAGTTTGGAT	TGTTTCCTTT	GTTGATTGAA	TTGACGAAAC	CAGAGGTTTT
90	100	110	120	130	140	150	160
CAAGACAGAT	AAGATTGGGT	TTATCAAAAC	GCAGTTTGAA	ATATTCCAGT	TGGTTTCCAA	GATATCTTGA	AGAAGATTGA
170	180	190	200	210	220	230	240
CGATTTGAAA	TTTGAAGAAG	TGGAGAAGAT	CTGGTTTGGA	TTGTTGGAGA	ATTTCAGAA	TCTCAAGATT	TACTCTAACG
250	260	270	280	290	300	310	320
ACGGGTACAA	CGAGAATTGT	ATTGAATTGA	TCAAGAACAT	GATCTTGGTG	TTACAGAACAA	TCAAAGTTCTT	GGACCAGACT
330	340	350	360	370	380	390	400
GAGAAATGCCA	CAGATATACA	AGGCGTCATG	TGATAAAATG	GATGAGATTT	ATCCCACAAT	TGAAGAAAAGA	GTTTATGGAA
410	420	430	440	450	460	470	480
AGTGGTCAAC	CAGAAGCTAA	ACAGGAAGAA	GCAAACGAAG	AGGTGAAACA	AGAAGAAGAA	GGTAAATAAG	TATTTTGTAT
490	500	510	520	530	540	550	560
TATATAACAA	ACAAAGTAAG	GAATACAGAT	TTATACAATA	AATTGCCATA	CTAGTCACGT	GAGATATCTC	ATCCATTCCC
570	580	590	600	610	620	630	640
CAACTCCCAA	GAAAAAATAA	AAGTGAAAAA	AAAAATCAA	CCCAAAGATC	AACCTCCCCA	TCATCATCGT	CATCAAAACCC

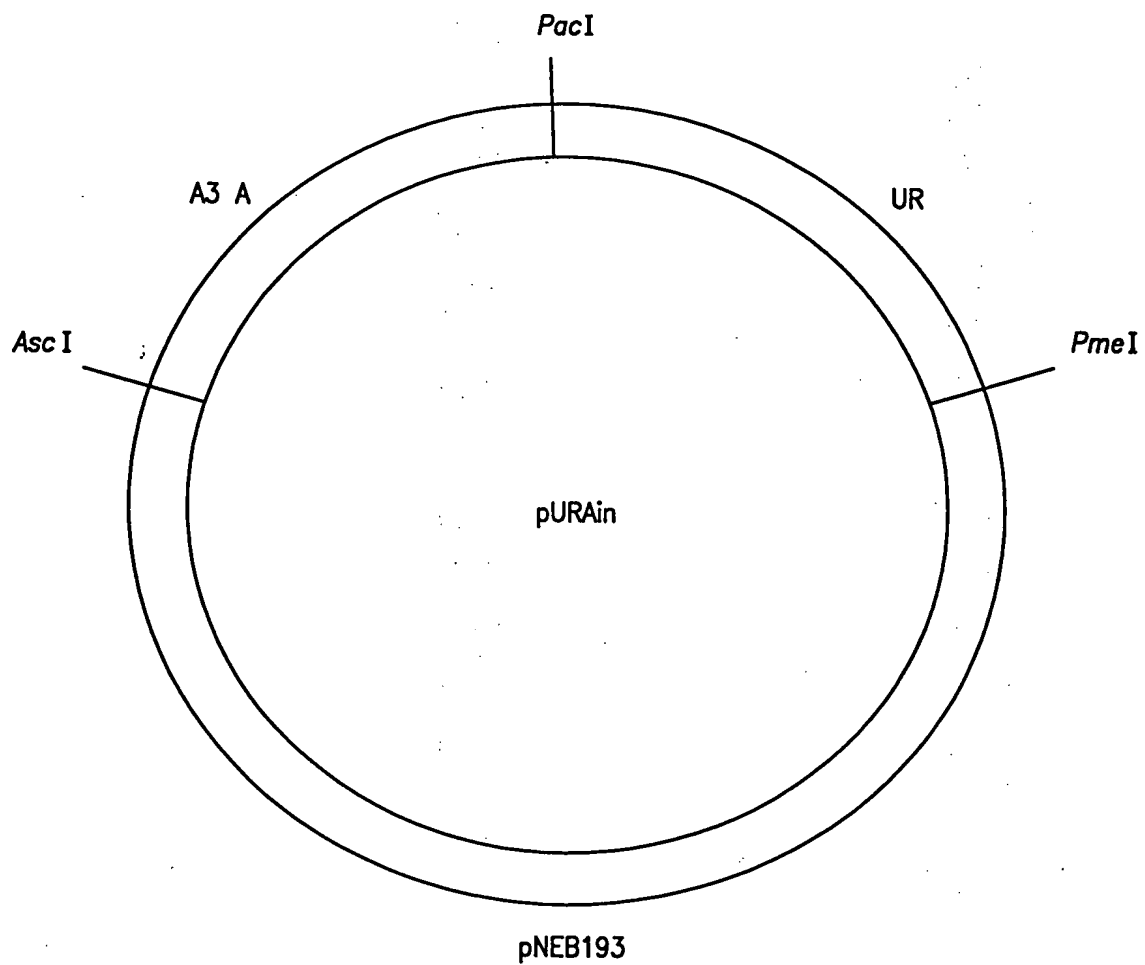
FIG. 23A

650	660	670	680	690	700	710	720
CCAGCTCAAT	TCGCAATGGT	TAGCACAAA	ACATACACAG	AAAGGGCATC	AGCACACCCC	TCCAAGGTTG	CCCAACGTTT
	M V	S I K	T Y T	E R A S	A H P	S K V	A Q R L>
730	740	750	760	770	780	790	800
ATTCCGCTTA	ATGGAGTCCA	AAAAGACCAA	CCTCTGCGCC	TCGATCGACG	TGACCACAAAC	CGCCGAGTTC	CTTTCGCTCA
	F R L	M E S	K K T N	L C A S	I D V	T T A	E F L S L>
810	820	830	840	850	860	870	880
TCGACAAGCT	CGGTCCCCAC	ATCTGTCTCG	TGAAGACGCA	CATCGATATC	ATCTCAGACT	TCAGCTACGA	GGGCACGATT
	I D K L	G P H	I C L	V K T H	I D I	I S D	F S Y E G T I>
890	900	910	920	930	940	950	960
GAGCCGTTGC	TTGTGCTTGC	AGAGGCCAC	GGTTCCTGA	TATTCGAGGA	CAGGAAGTTT	GCTGATATCG	GAAACACCCGT
	E P L	L V L A	E R H	G F L	I F E D	R K F	A D I G N T V>
970	980	990	1000	1010	1020	1030	1040
GATGTTGCAG	TACACCTCGG	GGGTATACCG	GATCGGGCGG	TGGAGTGACA	TCACGAACGC	GCACGGAGTG	ACTGGGAAGG
	M L Q	Y T S	G V Y R	I A A	W S D	I T N A	H G V T G K>
1050	1060	1070	1080	1090	1100	1110	1120
GGTTCGTTGA	AGGGTTGAAA	CGCGGTGCGG	AGGGGGTAGA	AAAGGAAAGG	GGCGTGTGTA	TGTTGGCGGA	GTTGTCGAGT
	G V V	E G L K	R G A	E G V	E K E R	G V L	M L A E L S S>
1130	1140	1150	1160	1170	1180	1190	1200
AAAGGCTCGT	TGGCGCATGG	TGAATATACC	CGTGAGACGA	TCGAGATTGC	GAAGAGTGAT	CGGGAGTTCG	TGATTGGGTT
	K G S	L A H G	E Y T	R E T	I E I A	K S D	R E F V I G F>

FIG. 23B

1210	1220	1230	1240	1250	1260	1270	1280
CATCGCGCAG	CGGACATGG	GGGTAGAGA	AGAAGGGTTT	GATTGGATCA	TCATGACGCC	TGGTGTGGGG	TTGGATGATA
I A Q	R D M	G G R E	E G F	D W I	I M T P	G V G	L D D>
1290	1300	1310	1320	1330	1340	1350	1360
AAGCGATGC	GTGGGCCAG	CAGTATAGGA	CTGTTGATGA	GGTGGTTCTG	ACTGGTACCG	ATGTGATTAT	TGTCGGGAGA
K G D A	L G Q	Q Y R	T V D E	V V L	T G T	D V I	I V G R>
1370	1380	1390	1400	1410	1420	1430	1440
GGGTTGTTTG	GAAAGGAAG	AGACCCTGAG	GTGGAGGGAA	AGAGATACAG	GGATGCTGGA	TGGAAGGCAT	ACTTGAAGAG
G L F	G K G R	D P E	V E G	K R Y R	D A G	W K A	Y L K R>
1450	1460	1470	1480	1490	1500	1510	1520
AACTGGTCAG	TTAGAATAAA	TATTGTAATA	AATAGGTCTA	TATACATACA	CTAAGCTTCT	AGGACGTCAT	TGTAGTCTTC
T G Q	L E	*>					
1530	1540	1550	1560	1570	1580	1590	1600
GAAGTTGTCT	GCTAGTTTAG	TTCTCATGAT	TTCGAAAACC	AATAACGCAA	TGGATGTAGC	AGGGATGGTG	GTTAGTGCCT
1610	1620	1630	1640	1650	1660	1670	1680
TCCTGACAAA	CCCAGAGTAC	GCCGCCCTCAA	ACCACGTCAC	ATTGCCCCCTT	TGCTTCATCC	GCATCACTTG	CTTGAAGGTA
1690	1700	1710					
TCCACGTACG	AGTTGTAATA	CACCTTGAAG	AA				

FIG. 23C



**FIG. 24**

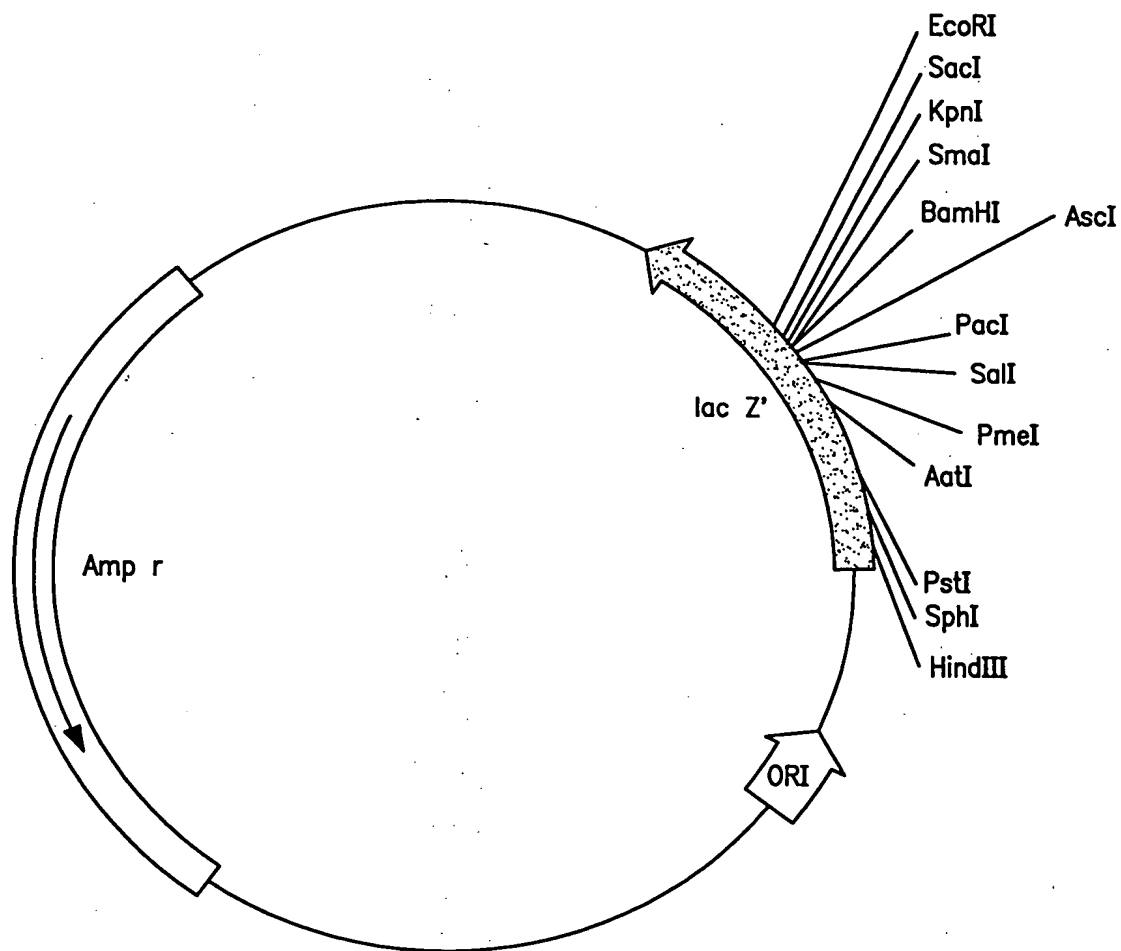


FIG. 25

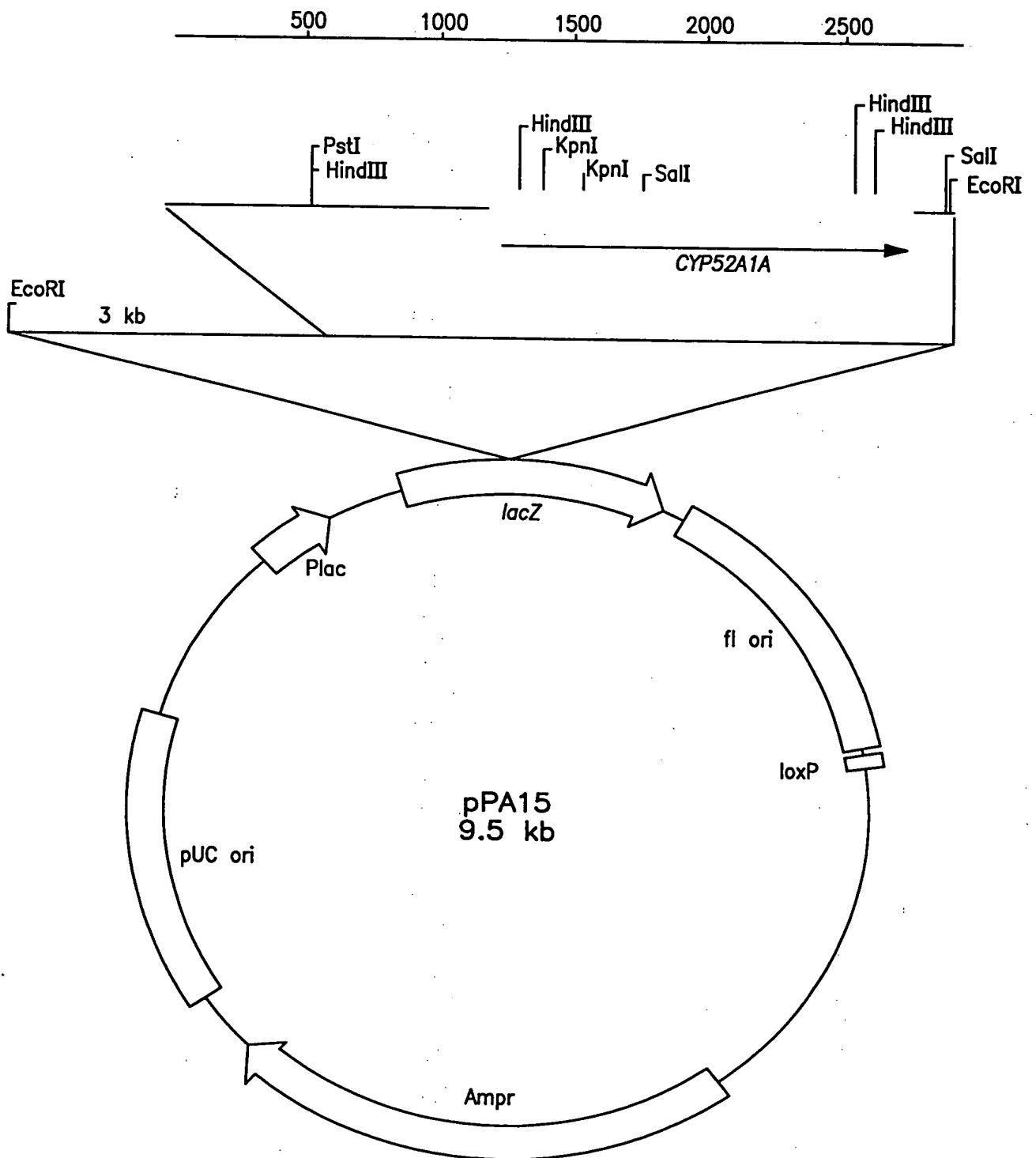


FIG. 26

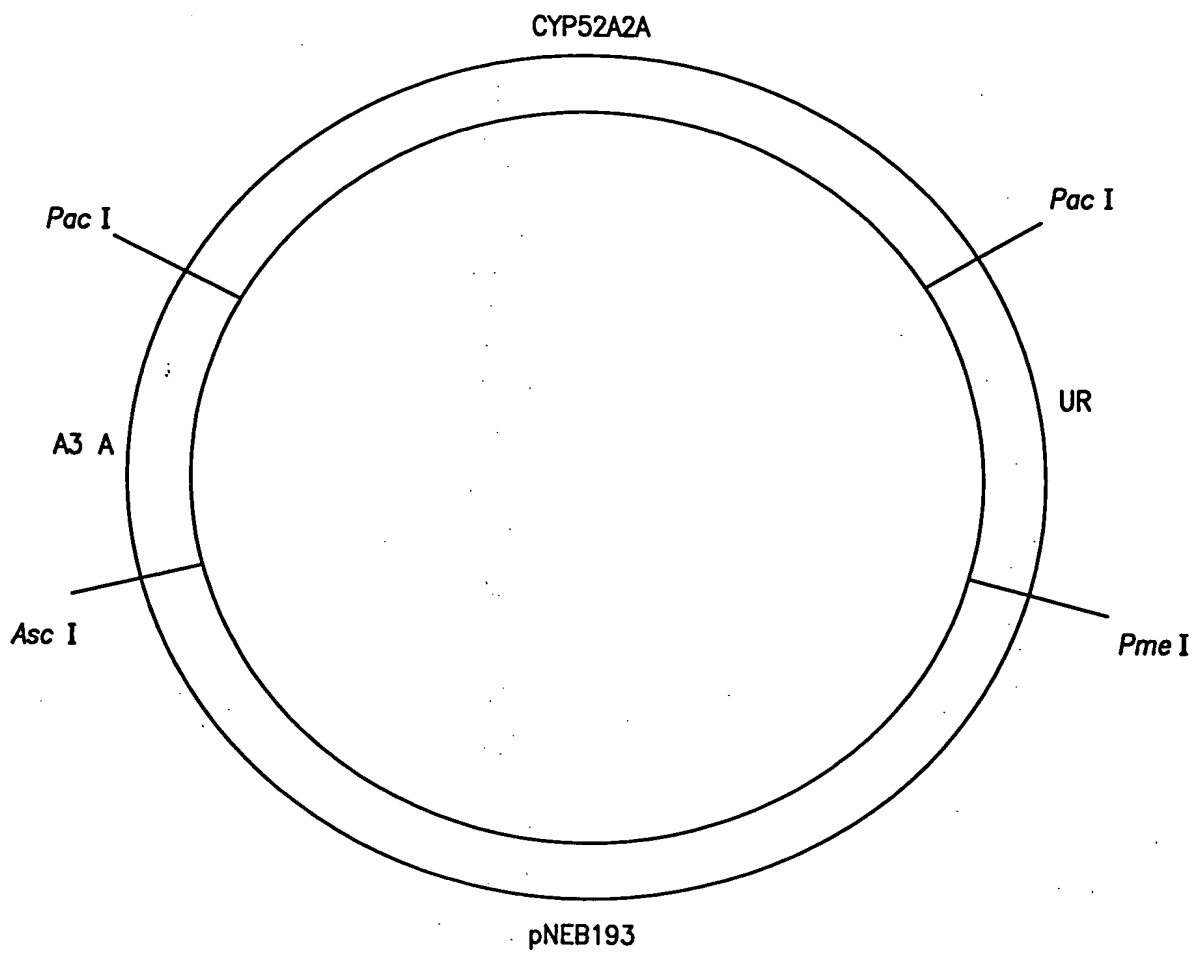


FIG. 27



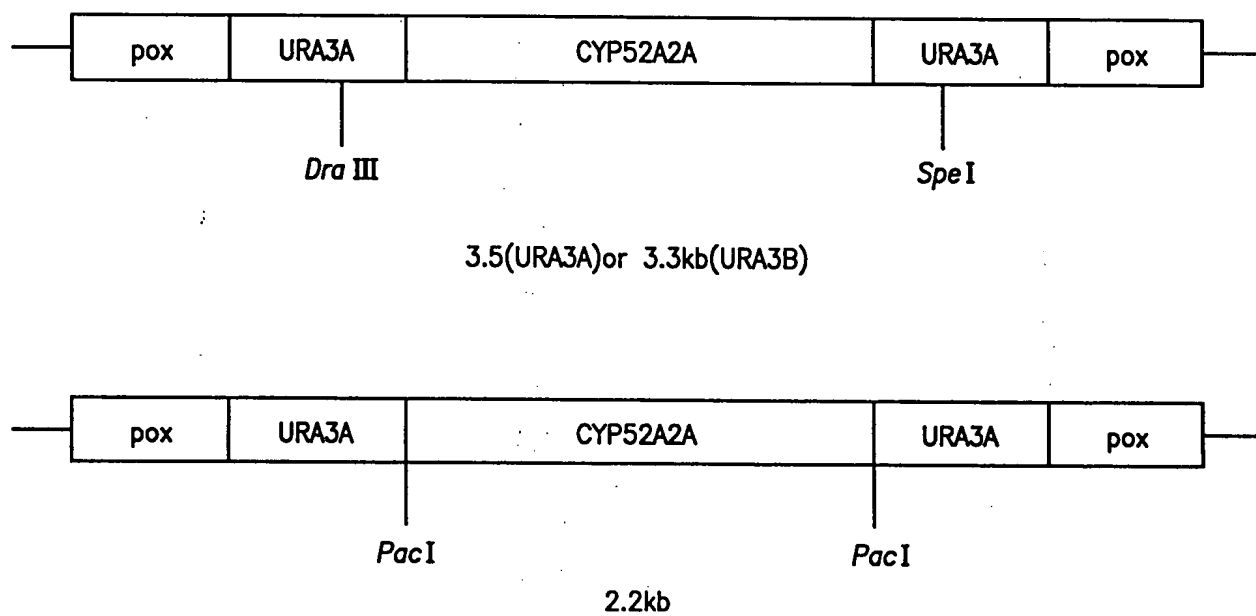


FIG. 28

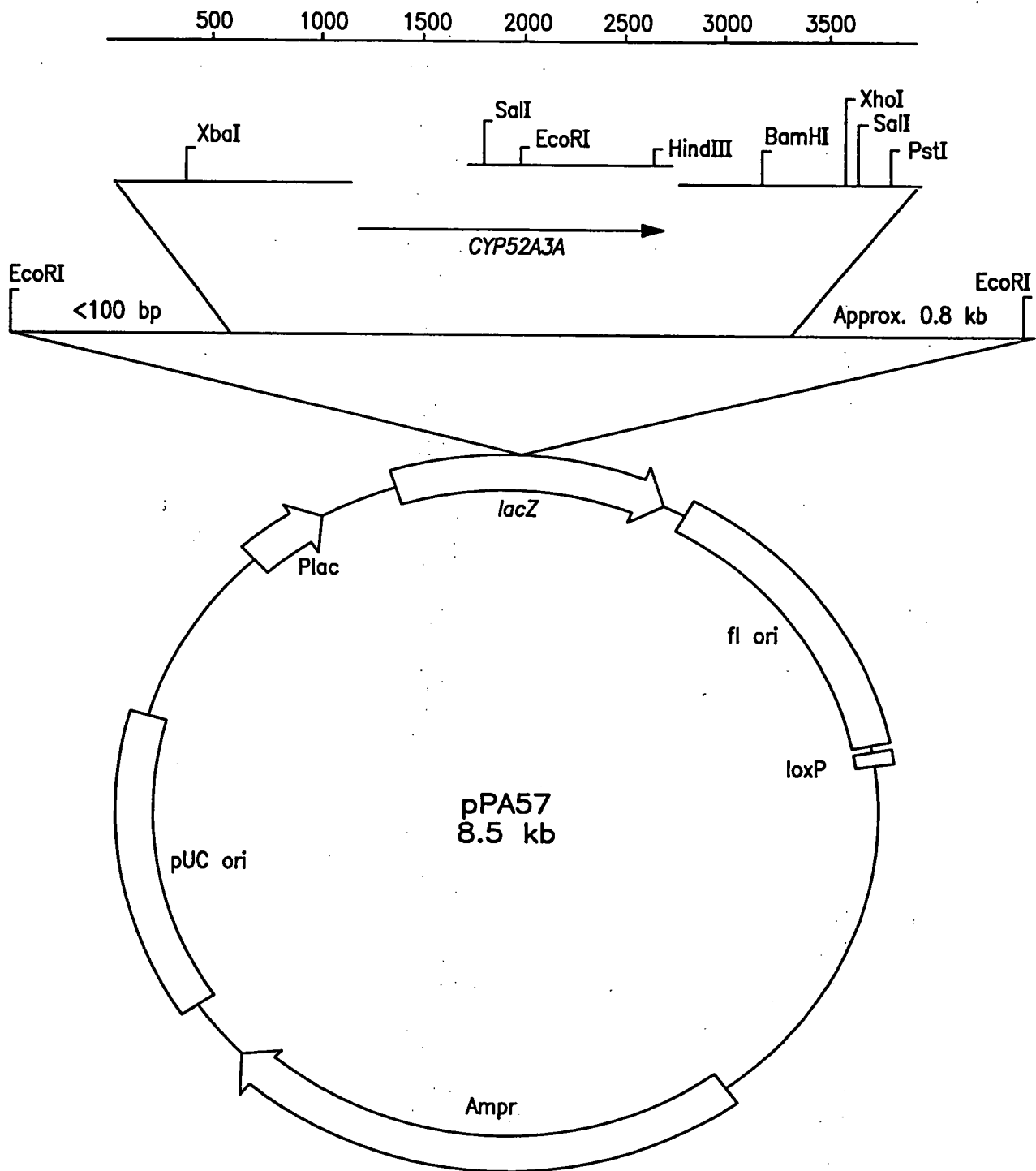


FIG. 29

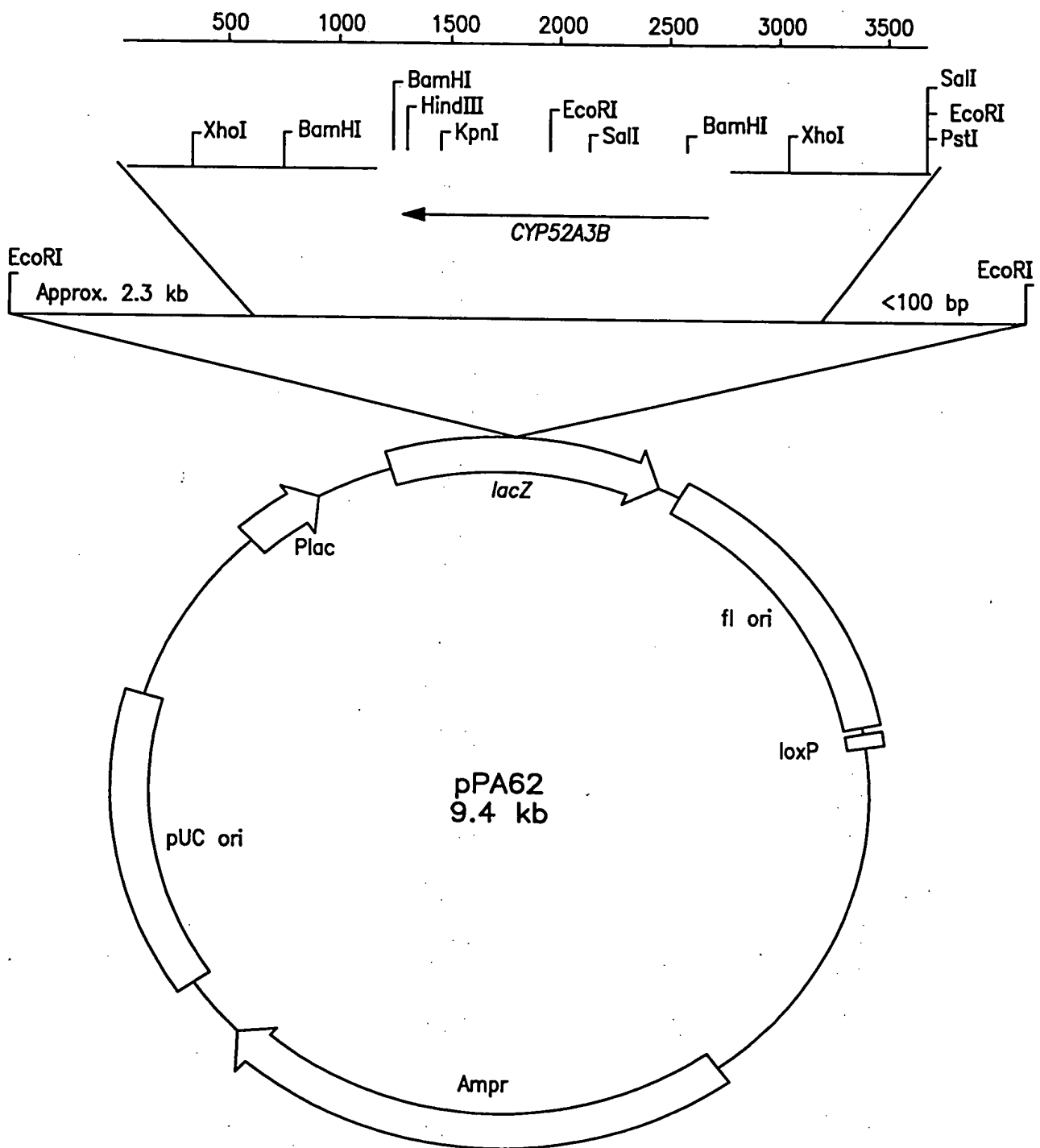


FIG. 30

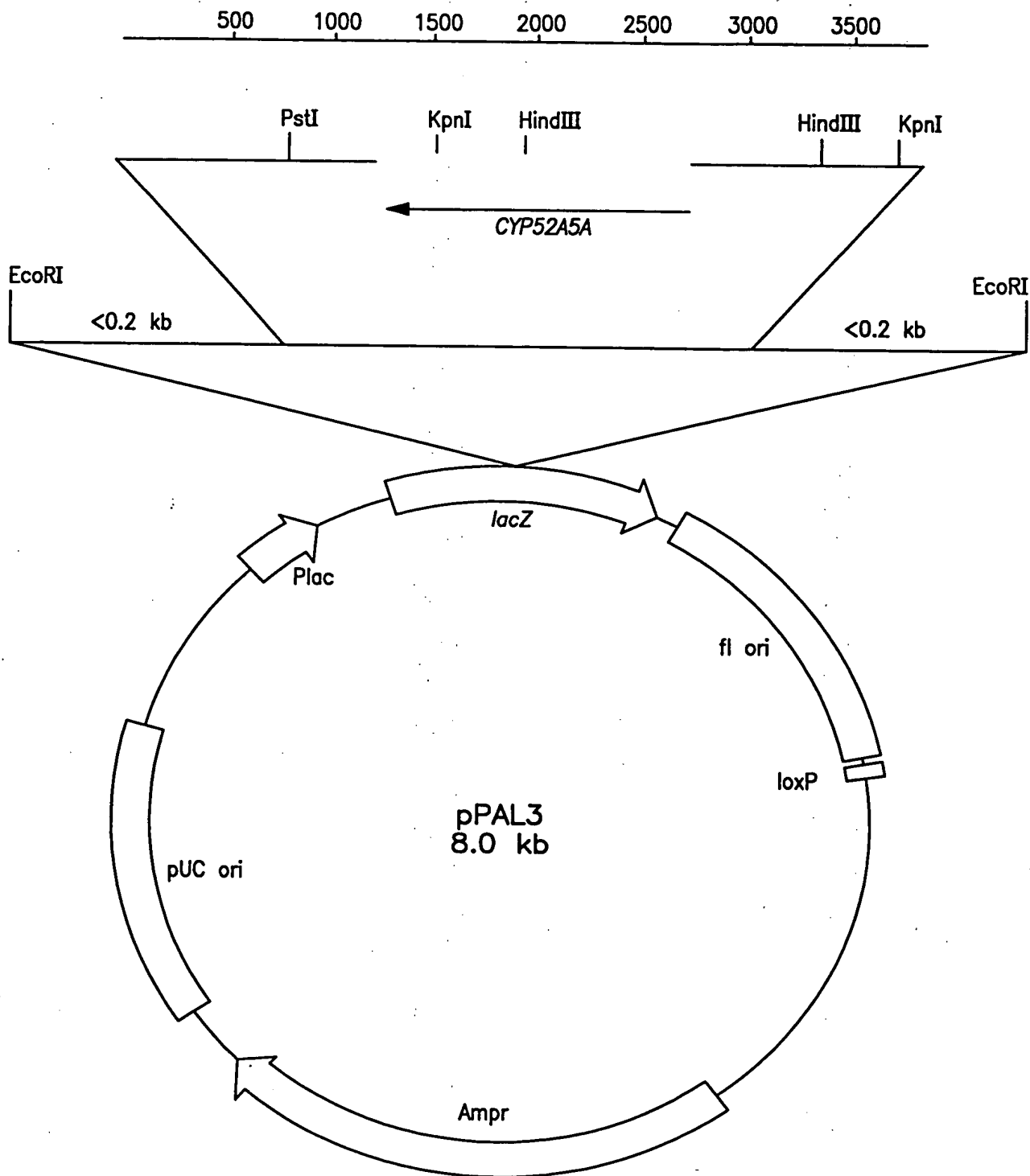


FIG. 3I

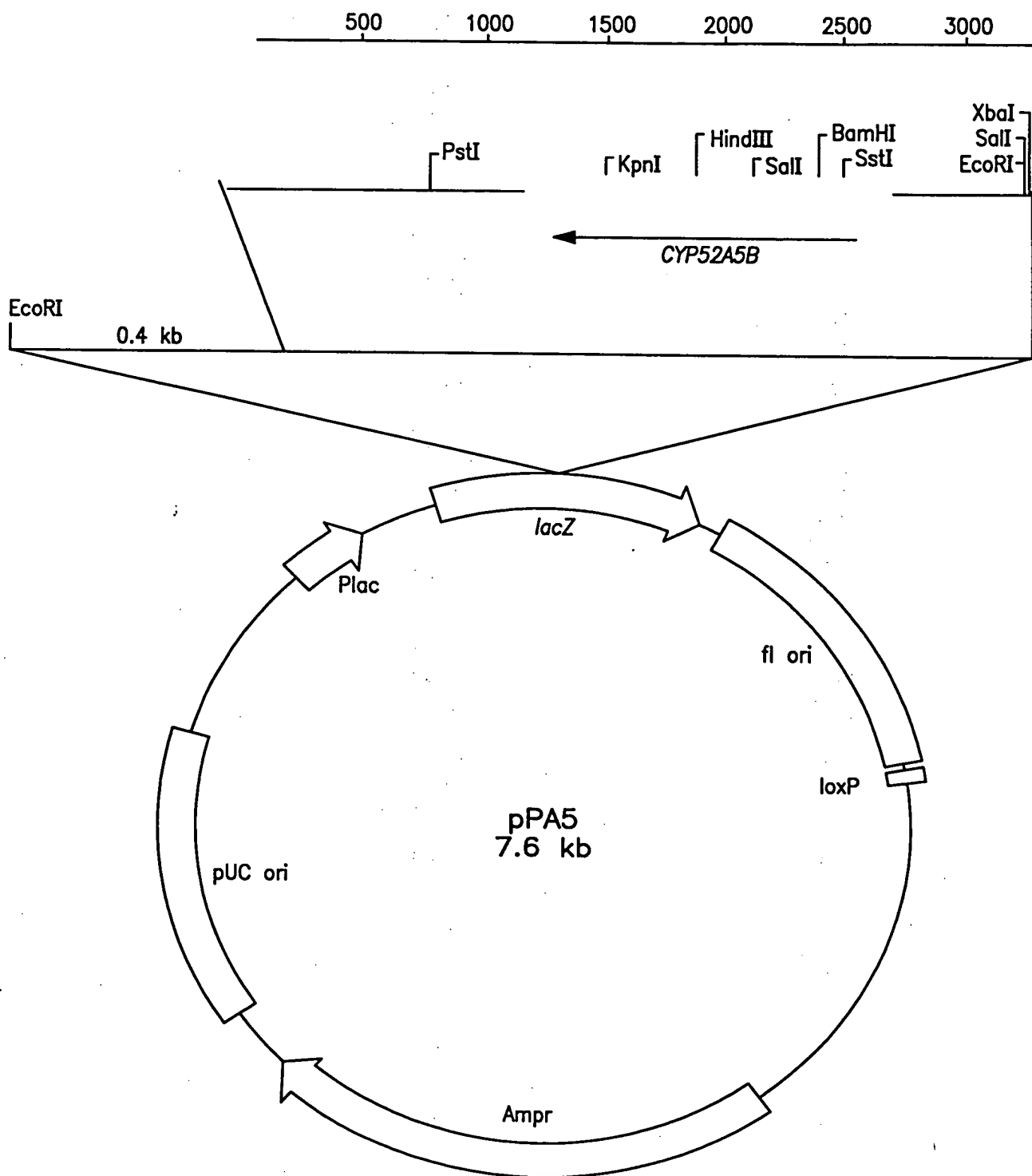


FIG. 32

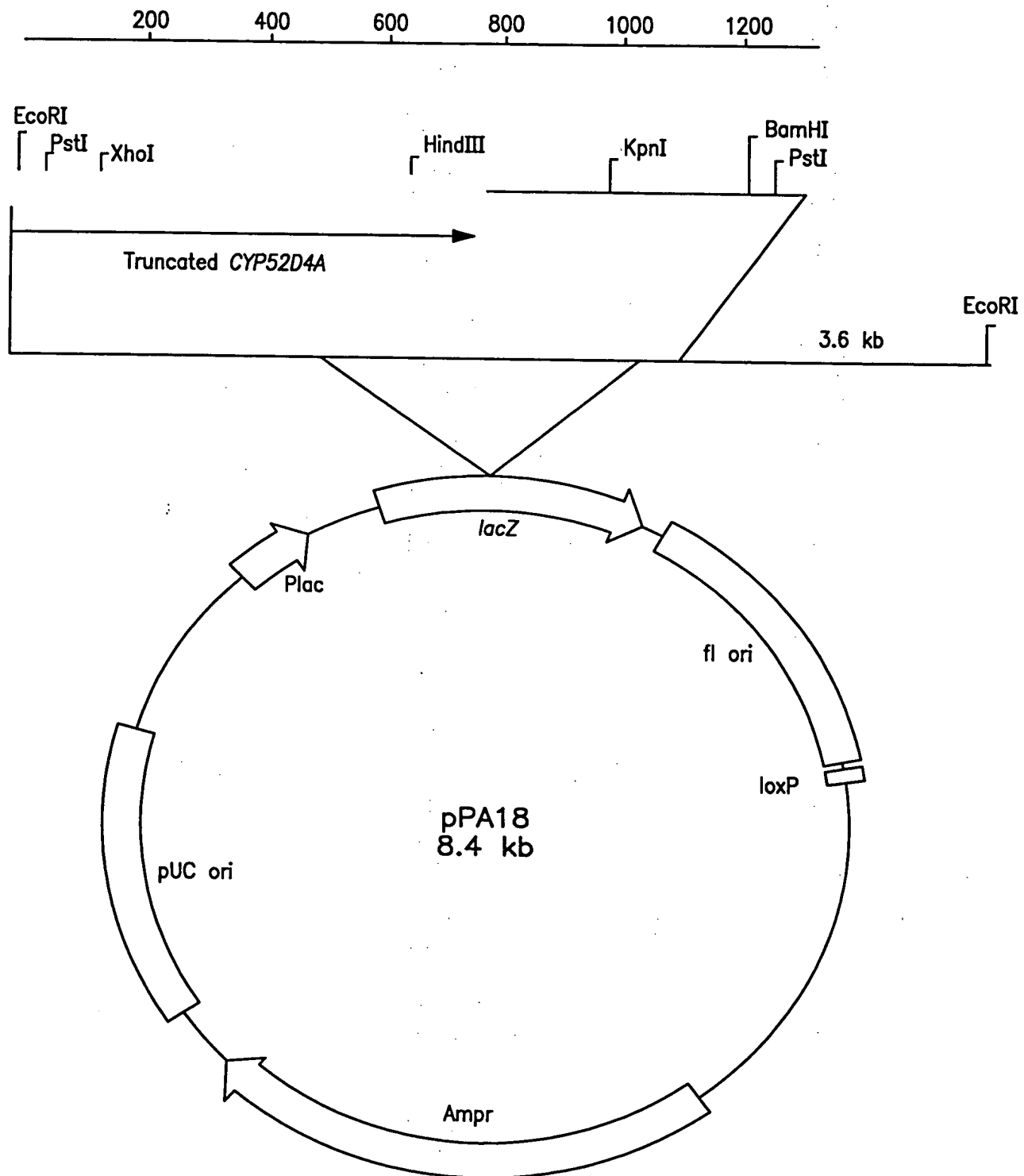


FIG. 33

### Expression of CYP52A1, CYP52A2 and CYP52A5 in Henkel Fermentor Run 3538-98

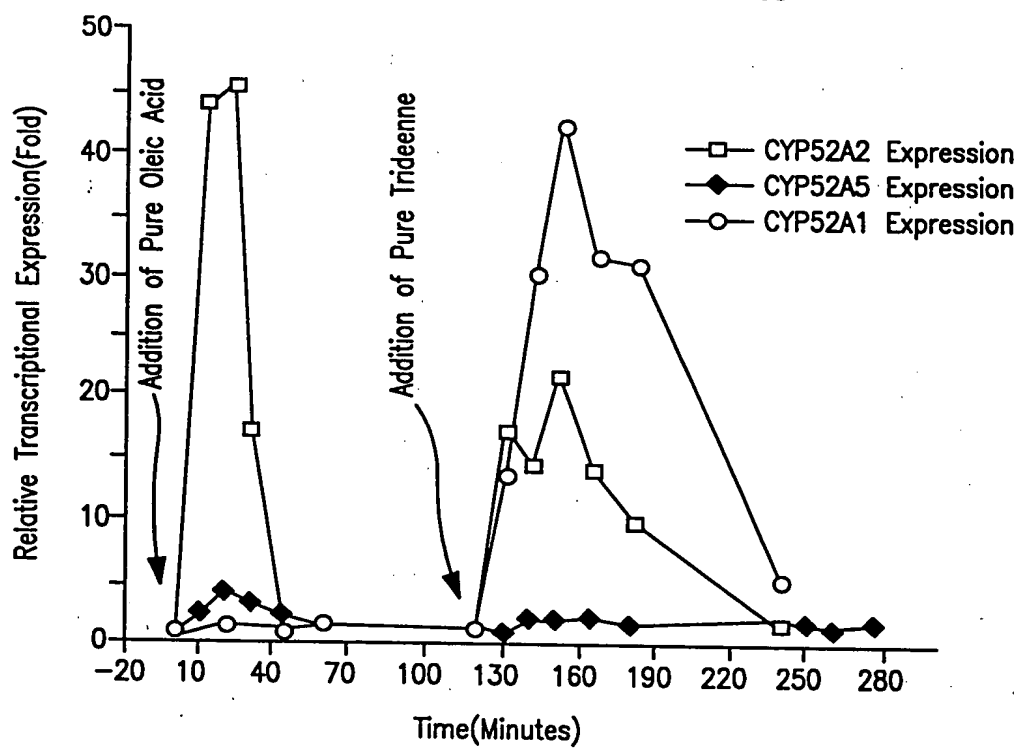
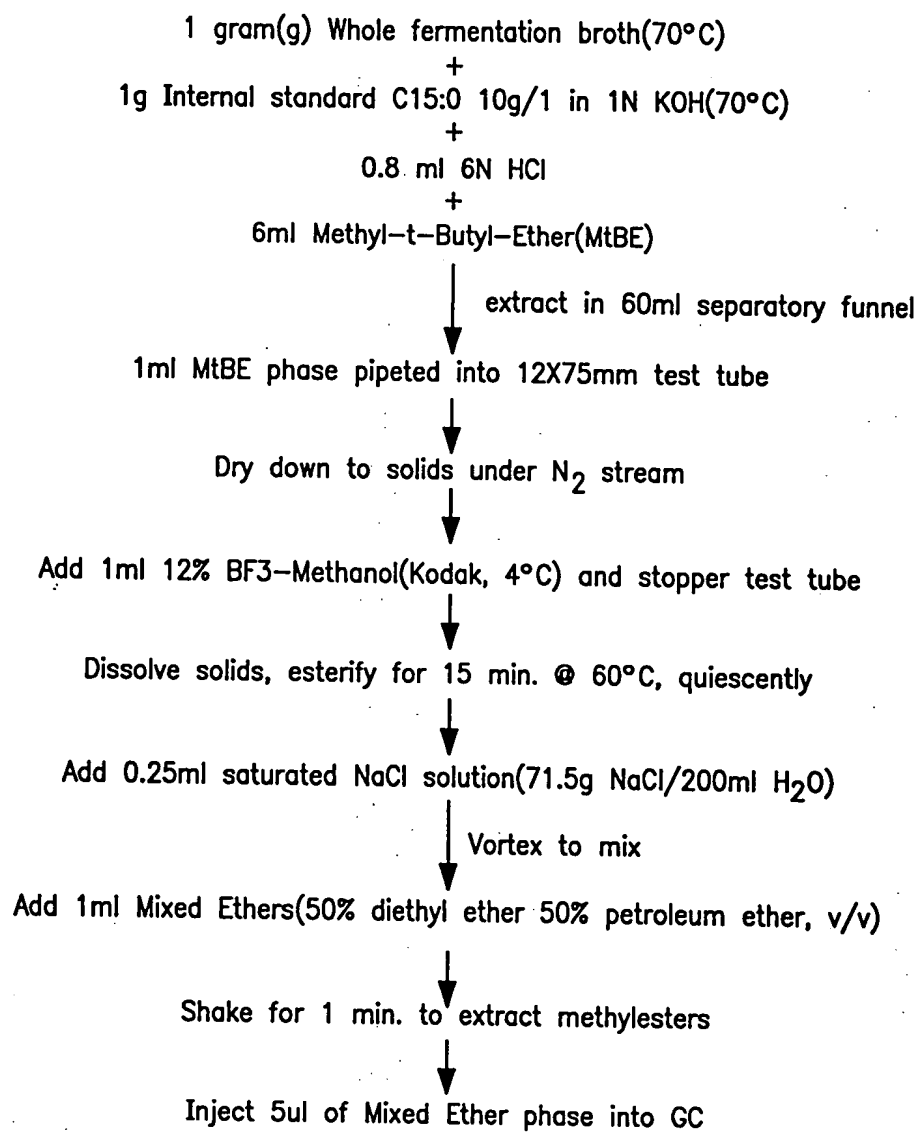


FIG. 34



#### GC parameters

Column : HP-INNOWAX capillary column, 30m X 0.32mm, 0.5  $\mu$ m film thickness  
 Split Ratio : 1:100

Column Head Pressure : 13.5 psig

Injector Temperature : 240°C

FID Detector Temp. : 250°C

Temp. Prog. : 90°C for 0 min. to 190°C @ 7°C/min. for 0 min. to 235°C @ 12°C/min. for 30 min.

**FIG. 35**



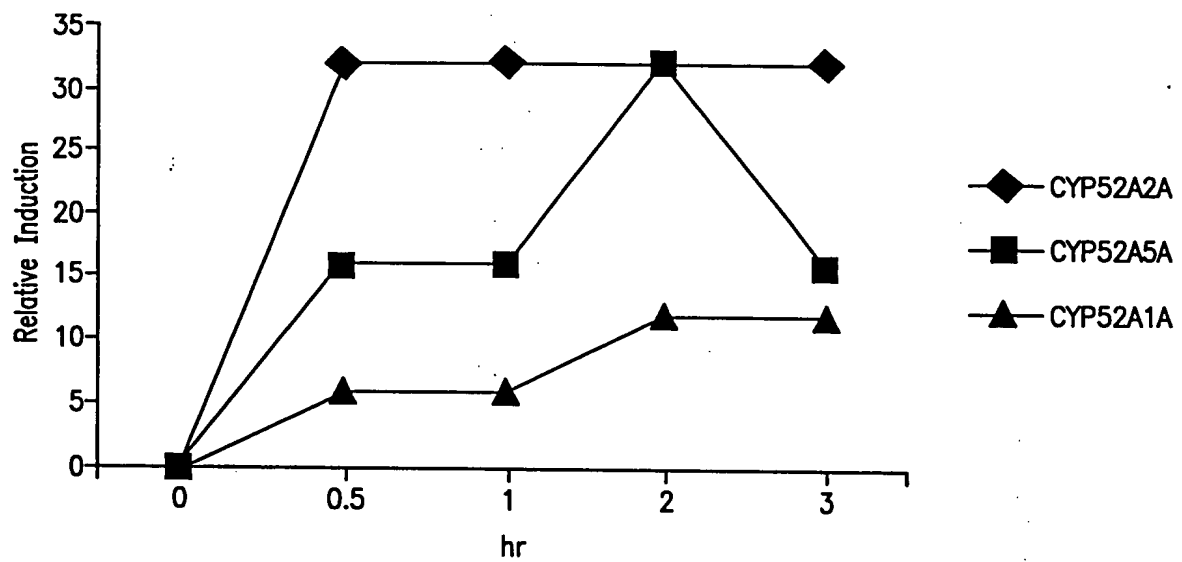


FIG. 36